PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C07K 14/79, A61K 38/40, G01N 33/68, A61K 7/16, 7/42

A1

(11) International Publication Number: WO 96/31537

(43) International Publication Date: 10 October 1996 (10.10.96)

(21) International Application Number: PCT/US96/04755

(22) International Filing Date: 5 April 1996 (05.04.96)

(30) Priority Data:

08/418,642	7 April 1995 (07.04.95)	US
60/000,819	27 June 1995 (27.06.95)	US
Not furnished	5 April 1996 (05.04.96)	US

(71) Applicant: THE PICOWER INSTITUTE FOR MEDICAL RESEARCH [US/US]; 350 Community Drive, Manhasset, NY 11030 (US).

(72) Inventors: LI, Yong, Ming; 61-52 165th Street, Fresh Meadows, NY 11360 (US). VLASSARA, Helen; Ram Island Drive, Shelter Island, NY 11964 (US). CERAMI, Anthony; Ram Island Drive, Shalter Island, NY 11964 (US).

(74) Agents: JACKSON, David, A. et al.; Klauber & Jackson, 411 Hackensack Avenue, Hackensack, NJ 07601 (US).

(81) Designated States: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, TR, TT, UA, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

With international search report.
Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION ENDPRODUCTS, AND METHODS OF THEIR USE

(57) Abstract

The present invention is directed to diagnostic and therapeutic methods based on the unexpected discovery that certain antibacterial proteins, in particular lysozyme and lactoferrin, bind to advanced glycosylation endproducts (AGEs) with high affinity, and that this binding activity is substantially non-competitive with binding of bacterial carbohydrates to the antibacterial proteins. Accordingly, the invention relates to methods for treating diseases and disorders associated with increased levels of AGEs, by administering a molecule having a hydrophilic loop domain, which domain in lysozyme and lactoferrin is associated with AGE-binding activity, and compositions comprising such a domain. The invention further relates to methods and compositions for partitioning AGEs away from a sample. The invention is also directed to methods for determining a prognosis of AGE complications in a patient suffering from an AGE-associated disease or disorder by measuring the level of activity of antibacterial proteins, such as lysozyme and lactoferrin, in a biological sample from a subject. Decreased levels of antibacterial protein bacteriocidal activity may be indicative of increased levels of AGEs, and a prognostic indicator of increased susceptibility to bacterial infection. In a further aspect, the invention relates to detection of AGEs in a biological sample. In specific embodiments, AGEs inhibit the bacteriocidal activity of lysozyme and lactoferrin, and 17 or 18 amino acid hydrophilic loop peptides bracketed by cysteine (the first and last amino acids are cysteine that form a disulfide bond) bind to AGE-bovine serum albumin.

IDS Reference AD
Serial No. 09/736,286
Int'l. Filing Date: August 23, 1999
Atty Docket: SHIM008

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgystan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic			SE	Sweden
CG	Congo	KR	Republic of Korea	SG	Singapore
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	LI	Liechtenstein	SK	Slovakia
CM	Cameroon	LK	Sri Lanka	SN	Senegal
CN	China	LR	Liberia	SZ	Swaziland
CS	Czechoslovakia	LT	Lithuania	TD	Chad
CZ	Czech Republic	LU	Luxembourg	TG	Togo
DE	Germany	LV	Latvia	TJ	Tajikistan
DK	Denmark	MC	Monaco	TT	Trinidad and Tobago
EE	Estonia	MD	Republic of Moldova	UA	Ukraine
ES	Spain	MG	Madagascar	UG	Uganda
FI	Finland	ML	Mali	US	United States of America
FR	France	MN	Mongolia	UZ	Uzbekistan
GA	Gabon	MR	Mauritania	VN	Viet Nam

AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION ENDPRODUCTS, AND METHODS OF THEIR USE

TECHNICAL FIELD OF THE INVENTION

The present invention generally relates to non-enzymatic glycosylation of proteins and particularly to agents that may be interactive with glycosylated proteins and that may affect the location and activity of such proteins. The invention further extends to compositions, materials including devices, and corresponding diagnostic and therapeutic methods that capitalize on the benefits of such agents.

BACKGROUND OF THE INVENTION

Advanced glycosylation endproducts (AGEs) represent a heterogeneous class of reactive products which form spontaneously *in vivo* from the non-enzymatic reaction of glucose and proteins (Monnier et al., 1981, *Science* **211**:491; Bucala et al., 1992, Advanced glycosylation endproducts, Harding and Crabbe, eds., In Post-Translational Modifications of Proteins, CRC Press Inc. **2**:53-79). Glucose and other reducing sugars react non-enzymatically with the amino groups of proteins in a concentration-dependent manner. Over time, these initial Amadori adducts undergo further rearrangements, dehydrations and cross-linking with other proteins to accumulate as a family of complex structures which are referred to as Advanced Glycosylation Endproducts (AGEs). Although this chemistry has been studied by food chemists for many years, it was only in the past decade that the presence of AGEs in living tissue has been established. The excessive deposition of these products on structural proteins as a function of age and elevated glucose concentration, taken together with evidence of effective prevention of tissue pathology by an AGE inhibitor, aminoguanidine, has lent support to the hypothesis that the formation of AGEs plays a role in the long term complications of aging and diabetes.

In vivo formation of AGE-proteins proceeds slowly under normal ambient glucose concentrations, while the rate of AGE accumulation is markedly accelerated in the

presence of hyperglycemia, as occurs in diabetes mellitus (Monnier and Cerami, 1983, *Biochim. Biophys. Acta* **760**:97-103; Monnier et al., 1984, *Proc. Natl. Acad. Sci. USA* **81**:583-87). Numerous studies suggest that AGEs play an important role in the structural and functional alterations which occur in senescence and long-term diabetes (Brownlee et al., 1988, *N. Engl. J. Med.* **318**:1315-1321).

Increased levels of AGEs in tissue and serum of hyperglycemic patients have been pathogenetically linked to numerous diabetic complications, such as vascular damage and nephropathy (Vlassara et al., 1994, *Lab. Invest.* **70**:138). Diabetic patients also exhibit increased susceptibility to bacterial infections; however, early studies failed to demonstrate a significant adverse effect of diabetes-associated metabolic disturbances, e.g. hyperglycemia, on defense system function or bacterial growth (Moutshen et al., 1992, *Diabetes and Metabolisme* **18**:187). We hypothesize that elevated levels of AGE may serve as a mediator to suppress normal defense in diabetic patients.

More generally, research on the binding properties and receptors for AGE-modified proteins has not heretofore identified a particular binding domain or motif responsible for AGE recognition, contact or binding. It is appreciated that such a discovery would greatly facilitate the development of effective strategies for both diagnostic and therapeutic modalities to deal with the adverse sequelae that have observed and extensively reported. It is therefore toward such a discovery that the present invention is directed.

SUMMARY OF THE INVENTION

In accordance with the present invention, a particular binding motif for advanced glycosylation endproducts (AGEs) has been determined with respect to endogenous antibacterial proteins. that is believed to represent more comprehensively, a focal point for the molecular control of AGE binding activity. As such, the present

invention contemplates the development of agents, compositions containing them, and a variety of uses that capitalize on this binding activity.

More particularly, the conserved binding motif comprises a common 17-18 amino acid cysteine-bounded hydrophilic peptide loop domain, initially discovered and identified in the antibacterial proteins lysozyme and lactoferrin. These cysteine loop domains have been prepared synthetically as described herein, and demonstrate AGE-binding activity. The particular cysteine-bounded loop domain is a common 17-18 residue hydrophilic loop ($CX_{15\text{-}16}C$) which has been named herein an AGE-binding cysteine-bounded loop domain or "ABCD" motif. The immediate utility of this structure is in the measurement of AGE levels in tissues and body fluids and the treatment of conditions characterized by aberrant AGE presence and activity generally and specifically, in relation to bacterial infection.

Therapeutic uses of the binding motif, active fragments thereof and cognate molecules extend to the direct treatment of patients to overcome bacterial infection by assisting the action of antibacterial proteins such as lysozyme and lactoferrin. The same agents could be used in an extracorporeal fashion, such as in a suitable device using, for example, selectively permeable "dialyzing" membrane, to sequester and remove AGE peptides and AGE proteins from blood or serum. Blood supplies could be treated in this fashion to reduce AGE levels and to thereby further reduce the likelihood of infection by reducing the development of *in vivo* protein/tissue senescence. The agents of the present invention could function to opsonize AGE peptides and in this way assist in their *in vivo* clearance by the body's mechanisms.

A particular device and corresponding methods of use are included, which may conveniently be employed in conjunction with the performance of peritoneal dialysis. Such a device and its use is of specific advantage in the indirect removal of undesired advanced glycation products from the blood. The device includes a catheter assembly for implantation in the peritoneum of a patient to introduce and

deliver a dialysate such as a glucose solution to the peritoneal cavity. Means for the sequestration and removal of deleterious molecules associated with, or comprising the products of, the spontaneous reaction pathways of glucose and proteins, including those entities known as Advanced Glycation Endproducts (or AGEs), are included with the catheter assembly and are disposed for registry with the peritoneal space.

The AGE-binding motif of the present invention, including active fragments thereof and cognate molecules, may also be used in diagnostic assays including drug discovery assays, to identify other active agents that could act as modulators of AGE activity and presence. Devices are contemplated that would contain such agents and that could bind to and thereby sequester AGE proteins and peptides to remove them from the body. Other diagnostic uses contemplate the use of the binding motif as a binding partner in the same manner as an anti-AGE antibody, for the capture of AGE-modified proteins, peptides, and other biomolecules, as an adjunct in an imaging assay for AGE-containing plaques such as those found in patients suffering from Alzheimers disease or atherosclerosis. In this latter utility, molecules bearing the binding motif or an active fragment thereof would be able to localize to amyloid and like plaques and likewise to other regions of AGE accumulation, and thereby assist in their measurement. These applications will best be realized when the AGE-targeting function of the ABCD peptide, an active fragment thereof or a cognate molecule or congener which by molecular resemblence shares AGE-binding activity with the ABCD peptide is conjugated to a label or tag that facilitates detection of the AGE-target conjugates.

The binding affinity of the agents of the present invention could be put to a variety of nontherapeutic uses, including their incorporation into personal care and cosmetic products that capitalize on the binding to topically resident AGEs. Thus, skin colorants, mascara and tooth whitening agents may be prepared which are based on the attachment to the agents of the invention of the appropriate visual indicator or colorant.

Accordingly, it is a principal object of the invention to provide a binding motif for that is specific to proteins or other biomolecules that have undergone advanced glycosylation.

It is a further object of the present invention to provide agents comprising or containing the binding motif as aforesaid, that exhibit a broad scope of utility including diagnostic, therapeutic and cosmetic applications.

It is a still further object of the present invention to provide methods for reversing AGE-mediated inhibition of antibacterial proteins.

It is a yet further object of the present invention to provide a method as aforesaid which is characterized by the discovery and use of the binding affinity of lysozyme and lactoferrin for advanced glycosylation endproducts.

Yet a further object of the present invention is to provide a method for treating AGE complications by administering a molecule having the structure of a hydrophilic cysteine loop such as that found in lysozyme and lactoferrin to inactivate AGEs.

Yet a further object is to provide a method for treating pathologies in which the presence and activity of AGEs is implicated by administering a molecule or active fragment thereof having the structure of the hydrophilic cysteine loop such as that found in lysozyme and lactoferrin, including lysozyme or lactoferrin, to assist in the removal of the AGEs.

A still a further object of the invention is to provide pharmaceutical compositions comprising such a molecule having the structure of the hydrophilic cysteine loop such as that found in lysozyme and lactoferrin.

A further object of the present invention is to provide methods and associated devices for the removal of AGE-modified molecules from biological fluids such as the blood, capable of either indwelling and extracorporeal operation and practice.

Other objects and advantages will become apparent to those skilled in the art from a review of the ensuing description which proceeds with reference to the following illustrative drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 demonstrates the binding of AGE-BSA to lysozyme and lactoferrin. AGE-BSA was prepared and radiolabeled as previously described (Vlassara et al., 1986, *J. Exp. Med.* **164**:1301). Hen egg-white lysozyme and purified human lactoferrin (Sigma) were immobilized on nitrocellulose membrane at 3 μg/dot. The membrane was blocked with 1% BSA in binding and washing buffer (0.05% Tween-20, 1x PBS), and blotted with 1,000,000 cpm ^{125}I-AGE-BSA/dot (NEN, specificity: 2000 cpm/ng BSA). After wash, bound ^{125}I-AGE-BSA was determined by a γ-counter. A. Saturation curve of AGE-BSA binding to lysozyme and lactoferrin. The K_d determined by Scatchard analysis for lysozyme and lactoferrin are 5 and 30 x 10^{-8} M, respectively. Results are representative of at least three independent experiments. B. Competition of AGE binding to LZ or LF with BSA, AGE-BSA, AGE-ovalbumin, FFI-B, Glucosamine, heparin, fucoidan, keratan, chondroitin and polyglutamic acid (at approximately 50-fold concentration).

FIGURE 2 shows that AGE-BSA inhibits the antibacterial activities of lysozyme and lactoferrin. A. Inhibition of lysozyme enzymatic activity by AGE-BSA. Enzymatic activity of recombinant human lysozyme (Sigma) with different amount of AGE-BSA were determined by measuring the lysis of lyophilized *Micrococcus lysodeikticus* (ATCC 4698) with a turbidimetric assay under recommended conditions (Sigma). Lysozyme (4 μg/ml) was added to 1 ml substrate (0.015%

Micrococcus suspension in 66 mM K_2SO_4 buffer, pH 6.24) with or without addition of AGE-BSA or BSA at indicated concentrations and the A_{420} was determined by kinetic analysis. Data at log phase (3 minutes) are presented here. Similar results were observed at other time points. B. AGE-BSA abrogates bacterial agglutination induced by lactoferrin. Lactoferrin (150 μg), lactoferrin plus AGE-BSA (150 μg), or lactoferrin plus BSA (150 μg) were added to 1 ml of *Micrococcus* suspension (0.015%), and the agglutination was determined by immediate measurement of turbidity change at OD_{700}. AGE-BSA was also added to lactoferrin-agglutinated bacterial suspension to observe the reversal of agglutination. C and D. AGE-BSA inhibition of bactericidal activity of lysozyme and lactoferrin. Live *Micrococcus luteus* (ATCC 9341) at 2.5 x 10^{-5} CFU/ml in Nutrient Broth (DIFCO) were incubated with lysozyme or lactoferrin plus AGE-BSA, AGE-ovalbumin, or BSA at indicated concentrations. The minimal inhibitory concentrations (MIC) at these conditions were determined by visualized bacterial growth after 18 hours incubation at 30°C.

FIGURE 3 presents a map of lysozyme AGE-binding domains. Lysozyme was digested with cyanogen bromide (CnBr) or idosobenzonate (IBzo) as previously described (Mahoney et al., 1979, *Biochemistry* 18:38100). Digested peptides and intact proteins were diluted in reducing sample buffer and analyzed by SDS-PAGE over 15% or 25% gels, transferred onto nitrocellulose membranes which were then blocked with 1% BSA and probed with ^{125}I-AGE-BSA. Amido black-stained nitrocellulose membranes, autoradiographs of ligand blots, and predicted digestion maps are presented. A. Lysozyme digested with CnBr. B. Lysozyme digested with IBzo. C. The predicted digestion maps and AGE-binding domains.

FIGURE 4 shows a map of lactoferrin AGE-binding domains. Digestion of lactoferrin was performed as described in Figure 3 for lysozyme (Mahoney et al., *supra*). Amido black-stained nitrocellulose membranes, autoradiographs of ligand blots, and predicted digestion maps are presented. A. Lactoferrin digested with

CnBr. B. Lactoferrin digested with V8 Protease. C. The predicted digestion maps and AGE-binding domains.

FIGURE 5 presents evidence of a common AGE-binding cysteine-bounded loop (ABCD motif) within AGE-binding domains. A. Protein sequences of a common $CX_{15-16}C$ cysteine loop within the AGE-binding domains of lysozyme and lactoferrin are aligned. B. Hydrophilicity analysis of these peptides using the Hopp-Woods method (analyzed with MacVector 4.0 software, IBI, New Haven, CT) . C. ^{125}I-AGE-BSA ligand dot blot. Peptides corresponding to the cysteine loops of lysozyme (LZ-C1, SEQ ID NO:7) and lactoferrin (LF-C1, SEQ ID NO:8) were commercially synthesized (Bio-Synthesis, Inc. Lewisville, TX). LZ, LZ-C1, LF-C1, an unrelated 28 amino acid peptide, and insulin were immobilized on nitrocellulose membrane at 30 μg/dot under reducing conditions. The membrane was blocked with 1% BSA in PBS buffer and blotted with 1,000,000 cpm ^{25}I-AGE-BSA for 1 hour in the presence (right column) or absence (left column) of 50-fold excess AGE-BSA. An autoradiograph is shown.

FIGURE 6 demonstrates detection of AGE-BSA using a sandwich-type ELISA-based assay. Lysozyme immobilized on the assay plate captured AGE-BSA from the sample and the level of detection was related to the concentration of AGE-BSA in the sample. Chicken lysozyme was reduced by addition of 2-mercaptoethanol. Lysozyme was adhered to a plate and AGE-BSA was added alone or with either 2% normal goat serum (NGS), 2% BSA, or 0.2% BSA and incubated. Anti-AGE monoclonal antibody diluted in buffer with 2% NGS was added and allowed to incubate. Alkaline phosphatase-conjugated anti-mouse antibody and *p*-nitrophenyl phosphate were used to detect the presence of AGEs bound to lysozyme.

FIGURE 7 shows in U/ml (1 Unit is defined as the competetive activity of a 1:5 dilution of normal human serum against α-AGE antibody binding to an AGE-BSA coated plate) the amounts of AGE-BSA which bound and were eluted from a chromatographic column of lysozyme- or BSA-derivatized beads. Cyanogen

that higher levels AGEs inhibit the activity of such antibacterial proteins, thus rendering an individual more susceptible to bacterial infection.

The following terms are defined to the extent that they may appear herein.

The term "a molecule having a hydrophilic cysteine-bounded loop domain", "a hydrophilic loop domain", or "motif", or other syntactic variants, refers to a compound of two or more subunit amino acids, amino acid analogs or peptidomimetics. The subunits may be linked by peptide bonds. In another embodiment, the subunit may be linked by other bonds, e.g., ester, ether, etc. As used herein the term "amino acid" refers to either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics. The molecule of the invention is constructed to have a structure corresponding to $R_1Xaa_1Xaa_nXaa_2R_2$. Xaa_1 and Xaa_2 are amino acids capable of forming a cross link, such as cysteine or glutamic acid or aspartic acid and lysine. In particular, where Xaa_1 and Xaa_2 are each cysteine, the cysteine residues form or are capable of forming a disulfide bond. R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen. Xaa_n is any L- or D- amino acid; and n = 13-18. In specific embodiments, *infra*, the molecule is a polypeptide having 17 or 18 L-amino acids (including the cysteine residues designated Xaa and Xaa_2).

The term "antibacterial protein" as used herein refers to a protein that has bacteriocidal activities, *e.g.*, lysozyme and lactoferrin, and that contains a hydrophilic cysteine loop of from about 15 to about 20 amino acid residues, including the cysteines that form cystine and that bracket the other 13-18 residues. Other examples of antibacterial proteins of the invention include, but are not limited to, defensins, azurocidins, neutrophil antibiotics, and seroprocidins. Such proteins can be from any animal species, *e.g.*, mammalian (human, bovine, ovine, equine, caprine, porcine, canine, feline, murine, rat, etc.), avian (chicken, etc.), or other sources.

bromide-activated Sepharose 4B beads were derivatized with lysozyme and a control column was established using BSA-derivatized beads. The columns were loaded with AGE-BSA and washed thoroughly; AGE-BSA remained bound to the column. Specific elution of AGE-BSA from the lysozyme-column was achieved by addition of 0.1 N NaOH.

FIGURE 8 shows uptake of AGE-modified molecules by macrophages and that addition of lysozyme to medium containing labeled AGE-BSA causes an increase in uptake of AGE-BSA by macrophage cultures. Mouse macrophage cells were cultured with ^{125}I-labeled lysozyme, -BSA, or -AGE-BSA and in conjunction with 50-fold excess of either unlabeled lysozyme, AGE-BSA, or both unlabeled lysozyme and AGE-BSA. Cells were incubated at 37°C for 2 h and then washed. A gamma-counter measured the amounts of ^{125}I taken up by the cells.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to the discovery that a binding motif specific to advanced glycosylation endproducts (AGEs) exists, and correspondingly, extends to diagnostic and therapeutic uses to which the discovery may be put. More specifically, certain antibacterial proteins comprising this domain and others, in particular lysozyme and lactoferrin, bind to advanced glycosylation endproducts (AGEs) with high affinity, and this binding has been observed to be substantially incompatible with the antibacterial properties of these proteins. Accordingly, the invention relates to methods and associated materials and devices for treating diseases and disorders associated with increased levels of AGEs, and compositions for the same. The invention is also directed to methods and associated materials and devices for determining a prognosis of AGE complications in a patient suffering from an AGE-associated disease or disorder, directly by measuring AGEs, or indirectly by measuring the level of activity of antibacterial proteins, such as lysozyme and lactoferrin, in a biological sample from a subject. While not intending to be limited by any particular theory or hypothesis, it is believed

The term "hydrophilic" in conjunction with the molecule as defined above means that the overall character of the molecule is polar, and the molecule is water soluble. This results from inclusion of subunits of the molecule, *e.g.*, amino acid residues, with polar functional groups. For example, in the instance where the molecule is a polypeptide, choices for amino acid residues include those with cationic side chains (arginine and lysine), anionic side chains (aspartate and glutamate), and neutral polar side chains (asparagine, glutamine, serine, and threonine) (*see, e.g.*, Cantor and Schimmel, in *BIOPHYSICAL CHEMISTRY Part I: The Conformation of Biological Macromolecules*, W.H. Freeman and Company: San Francisco, 1980, pp. 41-53).

As used herein, the term "AGE-" refers to the compound which it modifies as the reaction product of either an advanced glycosylation endproduct or a compound which forms AGEs and the compound so modified, such as the bovine serum albumin (BSA). Thus, AGEs include, but are not limited to, AGE-proteins (such as BSA-AGE), AGE-lipids, AGE-peptides, and AGE-DNA. AGE-polypeptides or AGE-proteins can be formed *in vitro* or *in vivo* by reacting a polypeptide or protein with an AGE, such as an AGE-peptide, or with a compound such as a reducing sugar, *e.g.*, glucose, until the polypeptide or protein is modified to form the AGE-polypeptide or AGE-protein.

The term "glycosylation" is used herein to refer to the non-enzymatic reaction of reducing sugars with a nucleophile, in particular an amine group, on a polypeptide or protein, such as hemoglobin, a lipid, or DNA, which leads to formation of AGEs. These processes are well known in the art, as described above. Recently, the term "glycation" has become more favored to refer to non-enzymatic glycosylation processes. Thus, the term "glycosylation," as specifically defined herein, and "glycation" are equivalent.

A composition comprising "A" (where "A" is a single protein, cell, etc.) is substantially free of "B" (where "B" comprises one or more contaminating

proteins, cells, etc.) when at least about 75% by weight of the proteins (depending on the category of species to which A and B belong) in the composition is "A". Preferably, "A" comprises at least about 90% by weight of the A+B species in the composition, most preferably at least about 99% by weight. It is also preferred that a composition, which is substantially free of contamination, contain only a single molecular weight species having the activity or characteristic of the species of interest.

The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness, and the like, when administered to a human. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "pharmaceutically acceptable carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the compound is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water or aqueous solutions, such as saline solutions and aqueous dextrose and glycerol solutions, are preferably employed as carriers, particularly for injectable solutions. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

The phrase "therapeutically effective amount" is used herein to mean an amount sufficient to reduce by at least about 15 percent, preferably by at least 50 percent, more preferably by at least 90 percent, and most preferably prevent, a clinically significant deficit in the activity, function and response of the host. Alternatively, a therapeutically effective amount is sufficient to cause an improvement in a clinically significant condition in the host.

As stated above, the present invention is based, in part, on the discovery that lysozyme and lactoferrin, major endogenous antibacterial proteins, bind to glucose-modified proteins (AGEs) with high affinity. The invention is further based on the observation that AGE binding inhibits the enzymatic and bactericidal activity of lysozyme, and blocks or reverses the bacterial agglutination and bacterial killing induced by lactoferrin.

The invention is further based on the discovery that a conserved domain present in both lysozyme and lactoferrin, as well as other antibacterial proteins, mediates binding to AGE.. This domain contains a common 17-18 amino acid hydrophilic cysteine loop structure. Cysteine-bounded loops corresponding the lysozyme and lactoferrin were prepared synthetically, and these peptides demonstrated AGE-binding activity.

These data indicate that molecules containing the structure of a hydrophilic cysteine-bounded loop, preferably of 17-18 amino acids, can be used to inhibit AGE-mediated inactivation of antibacterial proteins that contain such hydrophilic cysteine loops. Furthermore, such molecules may be used to detect the presence of AGEs in a sample, to target various labels to AGE-modified molecules or tissues, to partition AGEs out of a sample (*e.g.*, during dialysis), and to block the cross-linking activity of AGEs.

In particular it has been found that lysozyme binds to glucose-modified proteins, i.e. thouse bearing advanced glycosylation endproducts (AGEs), with a high affinity. AGE-BSA inhibits the enzymatic and bactericidal activity of lysozyme and blocks or reverses the bacterial agglutination and bacterial killing induced by AGE-binding lactoferrin. Mapping by proteolytic digestion revealed a single AGE-binding domain in lysozyme and two AGE-binding domains in lactoferrin. Within these domains, a common 17-18 amino acid hydrophilic cysteine loop ($CX_{15-16}C$) was found, that has been named AGE-binding cysteine-bounded domain or "ABCD" motif. Synthetic cysteine-bounded loop domains of lysozyme and

lactoferrin did exhibit AGE-binding activity. Similar loops are also present in other members of antimicrobial proteins. As set forth later herein, it is postulated that elevated levels of AGEs in tissues and sera of diabetic patients inhibit endogenous antibacterial proteins by binding to this conserved motif, and thereby increase the susceptibility to bacterial infections.

To provide a more complete understanding of the invention, the specification is divided into these various aspects of the invention. and sections relating to therapeutics and diagnostics.

Molecules Containing a Hydrophilic Loop Domain

According to the present invention, a molecule having a hydrophilic loop structural domain, which molecule binds to AGEs, can be prepared and used. In specific embodiments, *infra*, polypeptides having the amino acid sequences depicted in FIGURE 5A (SEQ ID NO:7, SEQ ID NO:8 and SEQ ID NO:9) have been prepared. These polypeptides are observed experimentally to bind to AGEs. Peptides or peptide analogs (*i.e.*, molecules containing non-peptidyl bonds, non-naturally occurring amino acids, and the like, but that have similar structural, physical, and chemical properties of peptides) can be prepared synthetically, *e.g.*, using the well known and highly developed solid phase condensation chemistry. Accordingly, the molecule can be prepared from L- or D- amino acids, polyesters and polyethers, amino acid analogs, non-classical amino acids, peptidomimetics, and the like (*see* Lam et al., International Patent Publication No. WO 92/00252, which is specifically incorporated herein by reference).

The invention extends to other hydrophilic polypeptide loop domains, *e.g.*, loops formed with disulfide, lactam, lactone or other ring closing moieties. That is, the spacer hydrophilic subunits of such a molecule are bracketed with a subunit, *e.g.*, an amino acid, that provides a chemical functional group capable of crosslinking to cyclize the peptide after treatment to form the crosslink. Cyclization will be favored when a turn-inducing amino acid is incorporated. Examples of amino

acids capable of crosslinking a peptide are cysteine to form disulfides, aspartic acid to form a lactone or a lactam, lysine and glutamic acid or aspartic acid to form an ϵ-amino/γ- (or β-)acid amide, and a chelator such as γ-carboxyl-glutamic acid (Gla) (Bachem) to chelate a transition metal and form a cross-link. Protected γ-carboxyl glutamic acid may be prepared by modifying the synthesis described by Zee-Cheng and Olson (1980, *Biophys. Biochem. Res. Commun.* **94**:1128-1132). A peptide in which the peptide sequence comprises two amino acids capable of crosslinking may be treated, e.g., by oxidation of cysteine residues to form a disulfide (cystine) or addition of a metal ion to form a chelate, so as to crosslink and cyclize the peptide to form the hydrophilic loop.

Based on the peptides identified herein that bind to AGEs, the general structural motif of a molecule of the invention can be determined. Identification and screening of antagonists is further facilitated by determining structural features of the protein, *e.g.*, using X-ray crystallography, neutron diffraction, nuclear magnetic resonance spectrometry, and other techniques for structure determination. The structure of the hydrophilic cysteine loop domain of the invention can be analyzed by various methods known in the art. Structural analysis can be performed in part by identifying sequence similarity with other known proteins. The degree of similarity (or homology) can provide a basis for predicting structure and function of the loop.

For example, sequence comparisons can be performed with sequences found in GenBank, using, for example, the FASTA and FASTP programs (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* **85**:2444-48). As has been performed herein, a candidate polypeptide for a hydrophilic cysteine loop structure should be further characterized by a hydrophilicity analysis (*e.g.*, Hopp and Woods, 1981, *Proc. Natl. Acad. Sci. U.S.A.* **78**:3824). A hydrophilicity profile can be used to confirm that the sequence of the candidate polypeptide is hydrophilic. Manipulation, translation, and secondary structure prediction, as well as open reading frame prediction and plotting, can also be accomplished using computer

software programs available in the art. The invention further envisions quantitative structural determination of the hydrophilic loop domain. Specifically, nuclear magnetic resonance (NMR), infrared (IR), Raman, and ultraviolet (UV), especially circular dichroism (CD), spectroscopic analysis can be used to characterize the structural motif of the hydrophilic loop. In particular NMR provides very powerful structural analysis of molecules in solution, which more closely approximates their native environment (Marion et al., 1983, *Biochem. Biophys. Res. Comm.* **113**:967-974; Bar et al., 1985, *J. Magn. Reson.* **65**:355-360; Kimura et al., 1980, *Proc. Natl. Acad. Sci. U.S.A.* **77**:1681-1685). Other methods of structural analysis can also be employed. These include but are not limited to X-ray crystallography (Engstom, A., 1974, *Biochem. Exp. Biol.* **11**:7-13). More preferably, co-crystals of the hydrophilic loop and an AGE can be studied. Analysis of co-crystals provides detailed information about binding, which in turn allows for rational design of analogs of the hydrophilic cysteine loops found in, *e.g.*, lysozyme and lactoferrin. Computer modeling can also be used, especially in connection with NMR or X-ray methods (Fletterick, R. and Zoller, M. (eds.), 1986, Computer Graphics and Molecular Modeling, in *Current Communications in Molecular Biology*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York).

Alternatively, a peptide or polypeptide molecule according to the invention, including lysozyme and lactoferrin, can be produced recombinantly. The polypeptide or protein may be expressed by a compatible cellular colony. Thus, in accordance with this aspect of the present invention there may be employed conventional molecular biology and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (herein "Sambrook et al., 1989"); *DNA Cloning: A Practical Approach*, Volumes I and II (D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid Hybridization* [B.D. Hames & S.J. Higgins eds. (1985)];

Transcription And Translation [B.D. Hames & S.J. Higgins, eds. (1984)]; *Animal Cell Culture* [R.I. Freshney, ed. (1986)]; *Immobilized Cells And Enzymes* [IRL Press, (1986)]; B. Perbal, *A Practical Guide To Molecular Cloning* (1984).

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (*e.g.*, mammalian) DNA, and even synthetic DNA sequences. If the coding sequence is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence. Many coding sequences for antibacterial proteins, in particular lysozyme, lactoferrin, defensins, azurocidin, neutrophil antibiotics, and seroprocidins are known in the art (Gabay et al., 1993, *Opin. Immunol.* 5:97; Leher et al., *Annu. Rev. Immunol.* 11:105).

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences.

Therapeutic Methods and Compositions

As the hydrophilic cysteine loop domain appears to play a role in the recognition, and may also be involved with removal, of advanced glycosylation endproducts *in vivo*, the present invention contemplates therapeutic applications for molecules having the structure of the hydrophilic cysteine loop domain, including active fragments, mimics thereof, and cognate or congener molecules thereto. Thus, a molecule of the invention that contains or comprises a hydrophilic loop structure can be prepared for administration in various scenarios for therapeutic purposes, in

most instances to assist in reducing the antibiotic protein inhibitory activity, cross-linking activity, and even concentration, of AGEs *in vivo*.

Numerous therapeutic formulations are possible and the present invention contemplates all such variations within its scope. A variety of administrative techniques may be utilized, among them topical applications as in ointments, creams, gels, and lotions to be applied directly to a wound or sore, or on surgical and other topical appliances such as, surgical sponges, bandages, gauze pads, and the like. Such topical pharmaceutical compositions have particular use for the treatment of diabetic ulcers, where the antibacterial protein inhibitory activity of AGEs may be involved in delaying the healing process. Alternatively, such compositions may be administered by parenteral techniques such as subcutaneous, intravenous and intraperitoneal injections, catheterizations and the like.

Corresponding therapeutic utilities take advantage of the demonstrated activity of the present molecule containing a hydrophilic loop structure, active fragments, mimics, congeners, and cognates thereof, toward advanced glycosylation endproducts. Thus, to the extent that the *in vivo* recognition and removal of AGEs serves to treat ailments attributable to their presence in an excess concentration, the administration of the present molecule comprises an effective therapeutic method. In particular, the present molecules could serve to localize concentrations of AGE accumulation and to enhance their detection and removal. Such conditions as atherosclerosis with or without diabetes, diabetic nephropathy, renal failure and the like may be treated and/or averted by the practice of the therapeutic methods of the present invention. A specific strategy involves the ability of the present molecules to opsonize AGE peptides and to thereby facilitate their *in vivo* clearance and removal.

Average quantities of the active agent effective for a positive therapeutic outcome may vary between different individuals, and in particular should be based upon the

recommendations and prescription of a qualified physician or veterinarian, with an exemplary dosage regimen extending to up to about 25 mg/kg/day.

The molecule having a hydrophilic loop domain, fragments, mimics, congeners, and cognates thereof, may be prepared in a therapeutically effective concentration as a pharmaceutical composition with a pharmaceutically acceptable carrier, as defined above. Preferably, as noted above, the carrier is suitable for topical administration. Other compatible pharmaceutical agents may possibly be included, so that for example certain agents may be simultaneously co-administered. In a preferred aspect, an inhibitor of AGE-formation is administered with the molecule, so as to simultaneously induce removal of AGEs and inhibit formation of new AGEs.

Thus, the invention provides for administering a molecule having a hydrophilic loop domain and an agent that blocks the post-glycosylation step, *i.e.*, the formation of fluorescent or crosslinking chromophores whose presence is associated with, and leads to, the adverse sequelae of glycosylation. An ideal agent would prevent the formation of a chromophore and its associated cross-links of proteins to proteins and trapping of proteins on to other proteins. The ideal agent would prevent or inhibit the long-term, glycosylation reactions that lead to the formation of the late-stage advanced glycosylation end products that are a direct cause of AGE-associated pathology.

An inhibitor of the formation of AGEs includes compounds that react with a carbonyl moiety of an early glycosylation product. Representative of such advanced glycosylation inhibitors are aminoguanidine, lysine and α-hydrazinohistidine. In a specific embodiment, the inhibitor is aminoguanidine (AG) and derivatives thereof. Pharmaceutical compositions and methods involving AG and derivatives thereof are well known, as described in U.S. Patents No. 4,758,583, issued July 19, 1988; No. 4,908,446, issued March 13, 1990; No. 4,983,604, issued January 8, 1991; No. 5,100,919, issued March 31, 1992; No.

5,106,877, issued April 21, 1992; No. 5,114,943, issued May 19, 1992; No. 5,128,360, issued July 7, 1992; No. 5,130,324, issued July 14, 1992; No. 5,130,337, issued July 14, 1992; No. 5,137,916, issued August 11, 1992; No. 5,140,048, issued August 18, 1992; No. 5,175,192, issued December 29, 1992; No. 5,218,001, issued June 8, 1993; No. 5,221,683, issued June 22, 1993; No. 5,238,963, issued August 24, 1993; No. 5,243,071, issued September 7, 1993; and No. 5,254,593, issued October 19, 1993. Other inhibitors of AGE formation are described in U.S. Applications Serial No. 07/652,575, filed February 8, 1991; Serial No. 07/889,141, filed May 27, 1992; Serial No. 07/896,854, filed May 15, 1992; Serial No. 07/986,661, filed December 8, 1992; Serial No. 07/986,662, filed December 8, 1992; Serial No. 08/027,086, filed March 5, 1993; and Serial No. 08/095,095, filed July 20, 1993. Each of the foregoing patents and patent applications is specifically incorporated herein by reference in its entirety.

Another important aspect of the invention is use of a molecule having a hydrophilic loop domain, fragments, mimics, congeners, and cognates thereof, to partition AGEs from *in vivo* samples and thus remove the toxic AGEs. That is, a molecule of the invention can be used, *e.g.*, in dialysis, to clear AGEs from the blood. A particular advantage of the invention is that where such a molecule also has antibacterial properties, *e.g.*, lysozyme or lactoferrin, it inherently contributes antiseptic characteristics to a dialysis procedure. Thus, in one embodiment, the molecule of the invention is immobilized on a membrane, *e.g.*, a dialysis membrane, to bind to and remove AGEs from the blood.

In another embodiment, the invention provides a device for adsorbing AGEs from a biological sample. The device comprises a closed structure, which structure is fabricated of an AGE-permeable membrane. Disposed within such device are particles to which a molecule of the invention is irreversibly associated or immobilized. In a specific embodiment, a "tea-bag" arrangement is envisioned, wherein the device forms the tea-bag and contains particles capable of binding to AGEs. A similar device formed of polypropylene mesh is described in Houghten,

1985, *Proc. Natl. Acad. Sci. USA* **82**:5131-5135; and U.S. Patent No. 4,631,211. Such a device can be used *ex vivo* or implanted *in vivo* in a subject for whom removal of AGEs is desired.

A particular device that may be prepared in accordance with the invention, may be employed in conjunction with the performance of peritoneal dialysis, to effect the indirect removal of AGEs from the blood. By way of background, peritoneal dialysis is one form of treatment that is administered to patients suffering from the complications of kidney dysfunction, such as end-stage renal disease (ESRD). Specifically, peritoneal dialysis proceeds by the introduction of a dialysate solution containing glucose (dextrose) into the peritoneal cavity, thereby promoting the movement of toxic waste products and excess fluid from the blood into such solution by diffusion across the peritoneal membrane. Osmotic ultrafiltration is achieved by adding increasing concentrations of glucose to the dialysate solution to thereby draw water from the blood and tissues into the dialysate. Peritoneal dialysis is not encumbered by a membrane pore size restriction as in the instance of hemodialysis, and frequently larger molecules such as proteins may be transported.

A particular type of peritoneal dialysis known as continuous ambulatory peritoneal dialysis (CAPD) has recently been developed to treat patients with ESRD. In CAPD, dialysate solution is infused from collapsible plastic bags into the abdominal cavity, where it may remain for a period of time before being drained.

The underlying condition that is treated by peritoneal dialysis, ESRD, is among the sequelae and complications attributable to the development of diabetes mellitus. In turn, diabetes mellitus has recently been investigated from the standpoint of the hypothesis that nonenzymatic reactions occur between glucose and structural proteins (glycation or nonenzymatic glycosylation) which then exert dramatic effects on the acceleration of the onset and severity of complications secondary to disregulation of blood sugar and/or insulin. More particularly, the formation of

advanced glycosylation endproducts (AGEs) has been studied extensively in the past decade, giving rise to the hypothesis that the formation of AGEs is a major factor in the development and severity of the various diabetic conditions and complications.

The device useful in the performance of peritoneal dialysis includes a catheter assembly for implantation in the peritoneum of a patient to introduce and deliver a dialysate such as a glucose solution to the peritoneal cavity. Means for the sequestration and removal of deleterious molecules associated with, or comprising the products of, the spontaneous reaction pathways of glucose and proteins, including AGEs, are included with the catheter assembly and are disposed for registry with the peritoneal space. Such means include a matrix modified to present or display one or more adsorptive agents or binding partners with specificity for AGE-modified molecules, especially low molecular weight molecules, such as AGE-peptides and AGE-proteins, and particularly such agents or partners as are capable of forming a complex therewith that facilitates the removal of such AGE modifiers or AGE-modified molecules from the patient as an added feature of therapy. Because circulating low-molecular weight AGEs, like other toxins that build up in the blood if clearance mechanisms by the kidneys are compromised on an acute or chronic basis, will be passed to the peritoneal space by normal physiological processes, means for removing such AGEs from the peritoneal space will "indirectly" lower the concentration of circulating AGEs, with beneficial results to the patient.

The term "binding partners" is intended to extend generally to specific adsorbents, absorbents or binding antagonists to the antigen, such as antibodies and other cellular binding proteins or receptors for the antigen. Such antagonists described above may vary in their composition. In the instance of AGE binding partners, the antigens are AGEs and similarly undesired earlier glycation products; and such reactive glycation intermediates, glycation adducts and crosslinks may be found free or on peptides, molecules and cells. The binding partners include and may

comprise materials that function as receptors for AGEs or that comprise the AGE-recognition domains of such molecules, as well as materials such as anti-AGE antibodies (intact or cleaved and/or purified to provide the AGE recognition domain at a higher concentration), activated charcoal, particular charged groups including for example boronic acids, and the like that are capable of binding AGE-proteins and -peptides.

The binding partners may be capable of treatment after withdrawal from the peritoneal cavity to dislodge bound ligands and to thereby rejuvenate the sequestration means for repeated use. Suitable binding partners include the materials listed above, and may further include by way of nonlimiting example, agents such as those set forth in copending application Serial No. 08/418,642 by one of the inventors herein, and accordingly include use of one or more materials such as a molecule having a hydrophilic loop domain, fragments, mimics, congeners, and cognates thereof. A further advantage would obtain if such a molecule also has antibacterial properties, e.g., lysozyme or lactoferrin, as it would inherently contribute antiseptic characteristics to a dialysis procedure.

More particularly, the dialysis device of the invention includes a catheter assembly where the means for sequestration and removal comprises a separate filament or tube that is positioned within the catheter and which is adapted for telescopic movement and extension into registry with the peritoneum and withdrawal therefrom while the catheter remains implanted. The filament or tube may be coated or impregnated with the binding partner. The sequestration means may be extended and withdrawn for replacement and/or rejuvenation during dialysis and provides an adjunct treatment for the patient by seeking to reduce concentrations of *in vivo* AGEs.

Suitable agents include all manner of binding partners for AGEs, including antibodies, and other antagonists as well. The sequestration means may employ a pelletized or particulate medium such as beads or pellets, bearing or comprising

the binding partner. In such instance the particulate material may be contained within a receptacle such as a semi-permeable tube or pouch, or may be interconnected by one or more filaments in a "beads-on-string" array. The tube, pouch or array would be capable of insertion beyond the distal terminus of the catheter into the fluid ambient of the peritoneum. In such embodiment, the receptacle, array and the particulate material are sized to accommodate the sizes of the target ligands, so that binding of the ligands and retention within the receptacle is assured when the receptacle is later withdrawn from the peritoneal cavity.

In a further embodiment, the sequestration means may comprise or employ a plurality of vesicles prepared from a nontoxic, non-biodegradable, semipermeable material, and a quantity of the binding partner provided therein, either by coating thereon and/or in liquid form therein. The vesicles are porous to permit the ingress of AGEs, AGE-proteins and AGE-peptides of various molecular masses.

A method for preparing the vesicles or pellets of the present invention may be accomplished by several techniques of which an organic phase separation method is preferred. In this method, the polymer that forms the non-biodegradable vesicles is dissolved in a suitable solvent to form a solution. The binding partner is likewise prepared with a suitable solvent and the resulting solution is then added to the polymer solution with stirring to form a dispersion. Thereafter, a solvent is added to the dispersion that is miscible with the polymer solvent but is not a solvent for the polymer and is likewise not miscible with the binding partner solution or dispersion. This causes a phase separation during which the polymer forms vesicles containing the binding partner. Alternately, the binding partner may be incorporated within vesicles by coating as by soaking of the vesicles in a solution thereof followed by drying. Also, a heat sealing process may be used in some instances wherein the binding partner is first placed within semipermeable, hollow fibers. The fibers may be prepared, for example, from a polycarbonate resin, in a manner ensuring that the smaller AGE-modified peptides can enter but that the larger AGE binding partners cannot leave the hollow core. This

procedure is useful in the instance where the binding partner is of solid particulate form as in the instance of charcoal.

In an alternate embodiment, the sequestration means may comprise a filamentary structure such as a flexible rod, tape or fiber that has disposed on its distal end a plurality of fibrils in turn, adapted for extension radially outward when the rod or fiber is thrust fully into the peritoneal cavity in use. Such fiber and its associated fibrils are coated or otherwise associated with the binding partners of the invention so that maximum surface area and concomitant efficiency of sequestration may be achieved. Correspondingly, the catheter assembly may utilize a cuff or support that anchors it into the adjacent body tissue or to the indwelling catheter, to secure a fluid impervious interfit during dialysis. Such cuff may likewise be coated with the binding partners of the invention to immobilize any unwanted AGE molecules that may be present in this area.

The advantage of the invention lies in the ability to administer treatment for the removal of AGE molecules that exacerbate and accelerate the severity of kidney disease, including without limitation, the secondary complications to tissues and organ systems other than the kidney, as well as the pathophysiological responses that occur in conjunction with renal disease and/or compromised renal function, while assisting the patient in the management of the condition. The concept of the invention contemplates inclusion in all manner of dialysis devices, including such devices as are maintained on an ongoing basis as well as those that are applied periodically and intermittently.

Diagnostic Methods

In one aspect, the invention relates to detection of the level of bacteriocidal activity of endogenous antibacterial proteins in a subject, preferably a human, believed to be suffering from elevated levels of AGEs, and complications derivative thereof. In particular, a sample from such an individual can be tested for lysozyme or lactoferrin activity, or both. A decrease in the level of

antibacterial activity compared to the individual at an earlier time or a normal individual may be indicative of inhibition of the antibacterial proteins by AGEs. Such a diagnosis may be confirmed indirectly by detecting elevated levels of AGEs. A decrease in the level of endogenous antibacterial protein bacteriocidal activity is prognostic of greater susceptibility to bacterial infections.

Suitable samples for detection of the level of bacteriocidal activity of antibacterial proteins can be selected from saliva, mucous (*e.g.*, nasal and pulmonary), phlegm, wound exudate, and infected sore exudate, as well as blood, plasma, urine, cerebrospinal fluid, lymphatic fluid, and tissue.

Ligands capable of binding to antibacterial proteins according to the invention include, but are not limited to, AGE-BSA and OVA-AGE, prepared as described *infra*, and the compounds FFI and AFGP, individually and bound to carrier proteins such as the protein albumin. A carrier may be selected from the group consisting of carbohydrates, proteins, synthetic polypeptides, lipids, bio-compatible natural and synthetic resins, antigens and mixtures thereof.

The present invention seeks to diagnose or determine a prognosis of AGE-related complications, monitoring the course of progression or treatment of an AGE-associated disease or disorder, or monitor a therapy for an AGE-associated disease or disorder. Such conditions as age- or diabetes-related hardening of the arteries, skin wrinkling, arterial blockage, and diabetic, retinal and renal damage in animals all result from the excessive buildup or trapping that occurs as advanced glycosylation endproducts increase in quantity. Therefore, the diagnostic method of the present invention seeks to avert pathologies caused at least in part by the accumulation of advanced glycosylation endproducts in the body by monitoring the amount level of antibacterial protein bacteriocidal activity.

In yet another embodiment, the molecule of the invention can be used to detect the presence or level of AGEs in a sample, *e.g.*, as an adjunct to or in place of an

anti-AGE antibody as described in Bucala, U.S. Patent Application No. 07/956,849, filed October 1, 1992, entitled "IMMUNOCHEMICAL DETECTION OF *IN VIVO* ADVANCED GLYCOSYLATION ENDPRODUCTS," which is specifically incorporated herein by reference in its entirety.

Thus, both the molecule having a hydrophilic loop domain, fragments, mimics, congeners, and cognates thereof, and any binding partners thereto that may be prepared, are capable of use in connection with various diagnostic techniques, including immunoassays, such as a radioimmunoassay, using for example, a receptor or other ligand to an AGE that may either be unlabeled or if labeled, then by either radioactive addition, reduction with sodium borohydride, or radioiodination. These general procedures and their application are all familiar to those skilled in the art and are presented herein as illustrative and not restrictive of procedures that may be utilized within the scope of the present invention. The "competitive" procedure, Procedure A, is described in U.S. Patent Nos. 3,654,090 and 3,850,752. Optional procedure C, the "sandwich" procedure, is described in U.S. Patent Nos. RE 31,006 and 4,016,043, while optional procedure D is known as the "double antibody", or "DASP", procedure.

Various assay formats are also contemplated by the present invention for detecting the presence, and if desired, the amount, of AGEs using the molecule of the invention. For example, a direct "sandwich"-type ELISA can be performed. Blotting formats, in which all the proteins from a sample are blotted, *e.g.*, by electroblotting, on a solid support, such as nitrocellulose, for detecting the presence, and if desired, the amount of AGEs are also contemplated by the instant invention. In a specific embodiment, *infra*, after blotting the hydrophilic loop-containing peptides in a sample on nitrocellulose, AGE is detected using a labeled AGE.

The present invention includes assay systems that may be prepared in the form of test kits for the quantitative analysis of the extent of the presence of advanced

glycosylation endproducts. The system or test kit may comprise a labeled component prepared by one of the radioactive and/or enzymatic techniques discussed herein. such as an antibody or ligand, as listed herein; and one or more additional immunochemical reagents, at least one of which is capable either of binding with the labeled component, its binding partner, one of the components to be determined or their binding partner(s).

In a further embodiment of this invention, commercial test kits suitable for use by a medical specialist may be prepared to determine the presence or absence of AGEs. Such kits can also be used to determine the amount of AGEs in a sample. In accordance with the testing techniques discussed above, one class of such kits will contain at least labeled molecule having a hydrophilic loop domain. fragment, mimic, congener. or cognate thereof, and may include directions, depending upon the method selected. *e.g.*, "competitive", "sandwich", "DASP" and the like. The kits may also contain peripheral reagents such as buffers, stabilizers, etc.

Accordingly, a test kit may be prepared for the demonstration of the presence and activity of AGE comprising:

(a) a predetermined amount of at least one labeled chemically reactive component obtained by the direct or indirect attachment of a molecule having a hydrophilic loop domain to a detectable label, fragments. mimics and cognates thereof;

(b) other reagents; and

(c) directions for use of said kit.

All of the protocols disclosed herein may be applied to the qualitative and quantitative determination of AGEs and to the concomitant diagnosis and surveillance of pathologies in which the accretion of advanced glycosylation endproducts is implicated. Such conditions as diabetes and the conditions associated with aging, such as atherosclerosis and skin wrinkling represent non-

limiting examples. and accordingly methods for diagnosing and monitoring these conditions are included within the scope of the present invention.

The diagnostic uses of the molecules of the present invention extend to their use as part of drug discovery assays to identify agents that could serve in a like capacity. For example, the molecules may be used as a binding partner in the same manner as an anti-AGE antibody, for the capture of AGE-modified proteins and peptides, and as an adjunct in an imaging assay for AGE-containing plaques such as those found in patients suffering from Alzheimers disease and scrapie.

The invention contemplates a variety of uses not strictly diagnostic or therapeutic in purpose. For example, the affinity of the present molecules for AGEs commends their use in the formulation of personal care and cosmetic preparations that would contain the present molecule(s) having attached thereto a colorant or the like. Such preparations could be used for facial and eye make-up, face or body tan simulating solutions, and as tooth whiteners.

The present invention will be better understood from a consideration of the following illustrative examples and data.

EXAMPLE 1

The mechanism of diabetes-associated high susceptibility of infections remains unknown. Lysozyme and lactoferrin are two major non-homologous endogenous antibacterial proteins present in saliva, nasal secretion, mucus, and lysosomes of neutrophils and macrophages (Philips, *Sci. Am.* **215**:78; Anderson et al., 1992, *Nature* **344**:784; Reiter et al., 1969, *Nature* **216**:643; Tenovu et al., 1991, *Proc. Finn. Dent. Sco.* **87**:197). We hypothesize that elevated levels of AGE may mediate the suppression of certain normal host defense mechanisms in diabetic patients. The following example illustrates the ability of lysozyme and lactoferrin

to bind to BSA-AGE in a time-dependent manner thus providing a likely means to reverse the AGE-mediated inhibition of antibacterial proteins.

Using ^{125}I labeled glucose modified bovine serum albumin (AGE-BSA) as a probe, we found that chicken lysozyme and recombinant human lysozyme exhibit AGE-specific binding activity on Western ligand blot (Figure 1). Human lactoferrin, similar to bovine lactoferrin reported earlier (Shmid et al., 1992, *J. Bio. Chem.* **267**:14987), also binds to AGE-BSA. At 4°C, the binding of AGE-BSA to both lysozyme and lactoferrin is apparently time-dependent and reaches a plateau by 30 minutes (Figure 1A). The binding is also saturable with an increasing concentration of ^{125}I-AGE-BSA ligand (Figure 1A). The calculated disassociation constant (K_d) is 5×10^{-8} M for lysozyme and 25×10^{-8} M for lactoferrin. This binding between AGE-BSA and lysozyme or lactoferrin is an AGE-specific non-covalent interaction since binding can be competed with other AGE-modified proteins, but not by non-glycated carrier proteins, glucose, Amadori products, glucosamine, or polyanionic/polycationic molecules (Figure 1B).

Lysozyme lyses Gram positive and some Gram negative bacteria by specific cleavage of 1-4 ß linkage between N-acetylglucosamine and N-acetylmurimate which comprise the peptidoglycan backbone of the bacterial cell wall (Philips, *Sci. Am.* **215**:78). By using lyophilized *Micrococcus lysodeikticus* as a substrate, we found that AGE-BSA inhibited the enzymatic activity of recombinant human and chicken lysozyme in a dose-dependent manner (Figure 2A), whereas, non-AGE-modified BSA control did not alter the activity of lysozyme. However, this inhibition did not reach 100% with an increasing dose of AGE-BSA suggesting AGE may be an indirect competitor for the substrate of lysozyme. Similarly, human lactoferrin-induced agglutination of *Micrococcus lysodeikticus* (Soukka et al., 1993, *Archs Oral Biol.* **38**:227) was completed blocked or reversed by addition of AGE-BSA, but not by BSA (Figure 2B). The bactericidal activity of both lysozyme and lactoferrin was also inhibited by AGE-BSA as indicated by changing of minimal inhibition concentrations (MIC) of both proteins in the

presence of AGE-modified protein (Figure 2C,D). The addition of AGE-BSA or AGE-ovalbumin increased lysozyme MIC for *Micrococcus* by 125-fold. By titration of AGE-ovalbumin and lysozyme concentrations, the minimal inhibition molar ratio of AGE-ovalbumin over lysozyme was determined as 3:1. The foregoing data suggest the prognostic capability of the invention, as elevations in AGE correlate with increased risk of AGE-related conditions, and such elevations were and may be measured by the corresponding inhibition or inactivation of lysozyme and lactoferrin.

Although lysozyme and lactoferrin share bactericidal and AGE-binding activity, no apparent primary sequence homology exists between these two proteins. We mapped the AGE-binding domain in these two proteins by proteolytic digestion using cyanogen bromide (CnBr), V8 protease, or iodosobenzonate (IBzo). Digested peptides were electrophoresed through SDS-PAGE, transferred onto nitrocellulose membranes, and blotted with ^{125}I-AGE-BSA. Partial CnBr digestion of chicken lysozyme indicated neither the first 12 residues at the N-terminal nor the last 25 residues at the C-terminal are required for AGE binding (Figure 3A). Partial digestion with IBzo revealed that the smallest fragment, at ~3 kDa, does not have AGE-binding activity whereas the secondary smallest fragment, at ~5 kDa, still retains full AGE-specific binding activity (Figure 3B). Based on the specific digestion map of lysozyme by CnBr and IBzo, the AGE-binding domain is localized to a 4.6 kDa fragment from amino acid 62 to 105 (Figure 3C).

In contrast, digestion of human lactoferrin with CnBr resulted in both a 40 and a 10 kDa AGE-binding fragment (Figure 4A). Partial digestion of lactoferrin with V8 protease revealed three distinct AGE-binding fragments of 22, 8, and 6 kDa (Figure 4B). We have sequenced the N-terminal twenty amino acids of these three AGE-binding peptides and found that the 8 kDa peptide is localized at the N-lobe (a.a. #1-20) and the 6 kDa fragment is localized at the C-lobe (a.a. #605-625) of human lactoferrin. Additionally the 22 KDa peptide shares the same N-terminus with the 8 kDa fragment. CnBr and V8 protease digestion map and AGE-binding

results are summarized in Figures 3A-C, and we concluded that there are at least two domains in lactoferrin (8 kDa, a.a. #1-80; 5 kDa, a.a. #603-653) that exhibit AGE-binding activity (Figure 4C).

Although these AGE-binding domains in lysozyme and lactoferrin do not share homology in primary sequences, we identified a common 17-18 amino acid hydrophilic cysteine loop ($CX_{15-16}C$) in these AGE-binding peptides (Figure 5A). Hydrophilicity analysis indicated that these loops are all hydrophilic (Figure 5B). We named this putative AGE-binding cysteine-bounded loop domain an "ABCD" motif. Synthetic peptides corresponding to this ABCD loop of lysozyme (CNDGRIPGSRNLCNIPC, a.a. #62-78, SEQ ID NO:7) and lactoferrin (CFQWQRNMRKVRGPPVSC, a.a. #8-25, SEQ ID NO:8; and CLQ, a.a. #613-630) were constructed. These synthetic ABCD loop peptides, but not irrelevant control peptides, are capable of binding to ^{125}I-AGE-BSA in ligand blot analysis (Figure 5C).

Interestingly, it was reported recently that the N-terminal cysteine loops of human and bovine lactoferrin (39% homology) are the bactericidal domain (Bellamy et al., *Biochem. Biophys. Acta.* **1121**:130), which may explain why AGE-binding to this loop blocked the bactericidal activity of lactoferrin. We further identify that this motif is also present in other members of antimicrobial proteins, such as defensins, azurocidin, neutrophil antibiotics, and seroprocidins (Gabay et al., 1993, *Opin. Immunol.* **5**:97; Leher et al., *Annu. Rev. Immunol.* **11**:105). It is also known that most bactericidal proteins are hydrophilic, at least over certain domains. Without any limitation by way of mechanism, the fact that this AGE-binding cysteine loop is apparently conserved across species and among defense proteins, may be responsible for the bacterial binding properties of these defense proteins. Glucose-modified proteins, like AGEs, may mimic molecular structures of the bacterial wall and bind to antibacterial proteins such as lysozyme and lactoferrin. High AGE levels in tissues and body fluids could form interactions with antibacterial proteins thus interfering with normal defense functions.

EXAMPLE 2

INHIBITION OF BACTERIAL GROWTH BY LYSOZYME WITH OR WITHOUT AGEs

The following example provides evidence that the lysozyme-mediated inhibition of bacterial growth is compromised by AGE-complexes and, additionally, that the deleterious effect of AGEs on lysozyme activity may be overcome by the addition of lysozyme or a peptide derived therefrom. By administration of the peptide of the invention, or a similar derivative of lysozyme, the inhibition of lysozyme activity by AGE-complexes can be minimized through a titration of AGEs by the additional lysozyme or derivative thereof. Furthermore, titration of AGEs provides a general method of treating individuals suspected of increased levels of AGEs and would not only overcome inhibition of lysozyme activity by AGEs but also rescue other cellular components whose activities are diminished by AGE complexes *in vivo*.

Materials and Methods

Live *Micrococcus luteus* (ATCC 9341) at 2.5 x 10^{-5} CFU/ml in Nutrient Broth (DIFCO) was incubated with lysozyme at concentrations of 0, 2, 10, 50, 250, 1250 and 3000 μg/ml plus 1.5 mg/ml AGE-BSA, AGE-ovalbumin, or BSA. Bacterial growth for different cultures was determined and based on visible bacterial growth after 18 hours incubation at 30°C.

Results

Addition of lysozyme to the bacterial cultures was a requirement to prevent bacterial growth, whether media was supplemented with BSA, AGE-BSA or AGE-ovalbumin and is shown in Table 1 below.

TABLE 1

Dose-dependent Inhibition of Bacterial Growth by Lysozyme with or without AGEs

Lysozyme (μg/ml)	BSA	AGE-BSA	Age-Ovalbumin
3000	-	-	-
1250	-	-	-
250	-	-	-
50	-	-	+
10	-	+	+
2	-	+	+
0	+	+	+

Addition of AGE-BSA and AGE-ovalbumin to cultures required that larger amounts of lysozyme be added to overcome the AGE-mediated inhibition of lysozyme's bactericidal effects. Unmodified BSA did not show an antagonistic effect on the bactericidal activity of lysozyme. Concentrations of lysozyme greater than about 10 μg/ml were effective in re-establishing the activity of lysozyme in killing bacteria in cultures supplemented with AGE-BSA, while concentrations of over 50 μg/ml of lysozyme were necessary to obtain the same effect in AGE-ovalbumin supplemented cultures.

Discussion

This Example demonstrates that AGE-modified compounds are capable of inhibiting the normal bactericidal activity of lysozyme, shown by the inability of lysozyme to exhibit this activity at concentrations otherwise capable of producing the effect in the absence of AGE-modified compounds. Furthermore, this inhibition may be overcome by further addition of lysozyme, or an AGE-binding peptide derivative thereof, in a dose-dependent fashion. Thus, the administration

of lysozyme, or an AGE-binding peptide domain thereof, to individuals suspected of increased levels of AGE-modified compounds can provide for a reduction of AGE levels and/or a reversal of the deleterious effects on lysozyme or other cellular components affected by AGEs.

EXAMPLE 3

DETECTION OF AGE-MODIFIED COMPOUNDS THROUGH AN ELISA-TYPE BINDING ASSAY UTILIZING LYSOZYME

Detection of AGE complexes in a sample has great significance in determining pathological levels of AGEs in blood or tissue of a subject or in any biological sample. This Example demonstrates such a detection method by adhering lysozyme, or a peptide comprising the AGE-binding domain thereof, although any homologous peptide providing a similar region of AGE binding capability can be employed, to a surface and incubating or passing a sample over the peptide to allow it to capture the AGE-modified molecules of the sample. A detector antibody raised against AGEs then can be used to detect the presence of AGE-modified components specifically bound to the adhering lysozyme or the AGE-binding peptide domain thereof. The following details extend further to therapeutic application of this AGE binding activity, to facilitate the removal of, for example, AGE-peptides from blood and serum.

Materials and Methods

In a first series of experiments, chicken lysozyme was initially prepared in phosphate buffered saline (PBS) at a concentration of 30 mg/ml and reduced by addition of 2-mercaptoethanol at a final concentration of 2% (vol:vol). To adhere lysozyme to the ELISA plate, the reduced preparation of lysozyme was diluted in coating buffer (CB; 0.1 M $NaHCO_3$, pH 9.6, with 0.02% NaN_3 w/v) to a final concentration of 100 μg/ml. Aliquots of 100 μl of this preparation were then applied to each well of a 96-well ELISA plate at 4°C and incubated overnight to allow lysozyme to adhere to the plate. The plate was next washed three times in

Wash Buffer (WB; PBS with 0.05% Tween-20, 1 mM NaN_3) and blocked with 150 μl/well SuperBlock (Pierce, cat. #37515) at room temperature for 1 h. Again, the plate was washed three times with WB, and AGE-BSA diluted with dilution buffer (DB; 0.2% Tween in PBS at pH 7.4) was added alone or with either 2% normal goat serum (NGS), 2% BSA, or 0.2% BSA and incubated at room temperature for 2 h on a shaker. A dilution series of a standard preparation of AGE-BSA was added to wells in triplicate, in concentrations that varied from 0.01 μg/ml - 1000 μg/ml in increments of 10x. The specific activity of this AGE-BSA was approximately 1 Unit per 2.21 μg of AGE-BSA, assessed by a standard ELISA assay using a monoclonal anti-AGE antibody. After washing the plate with WB, an anti-AGE monoclonal antibody diluted with 2% NGS in DB was added and allowed to incubate at room temperature for 2 h with gentle shaking. The plate was washed 3x with WB and an alkaline phosphatase-conjugated anti-mouse antibody raised in goat or rabbit, for instance, (e.g. Cappel, cat. #59296), diluted 1:3000 in DB plus 1% NGS was added to the wells and incubated at 37°C for 1 h. The plate was next washed and 1 mg/ml of *p*-nitrophenyl phosphate in substrate buffer (SB; 9.7 ml diethanolamine, 0.1 g $MgCl_2 \cdot 6H_2O$, 0.2 g NaN_3 in 800 ml ddH_2O, pH 9.8, diluted to 1L with ddH_2O) was added. The OD was measured at 405 nm after addition of substrate and once the highest OD was reached (approximately 60 min.).

Results

Detection of AGE-BSA by this sandwich-type ELISA-based assay was related to the concentration of AGE-BSA in the sample, regardless of whether excess purified protein was included in the sample dilution buffer or not (see Figure 6). Interestingly, the apparent efficiency with which lysozyme captured and presented AGE-BSA in the sample to the detector antibody differed depending on the addition of BSA or NGS to the dilution buffer. When unmodified BSA was included in the sample dilution buffer in concentrations of 2% or 0.2%, the ability of lysozyme to detect AGE-BSA improved compared to parallel assays employing 2% NGS in DB or assays where sample dilution buffer was used alone. In all

cases lysozyme captured AGE-BSA from the sample, in proportion to the AGE-BSA concentration. allowing the detector antibody to bind to the complex, thus measuring levels of AGE-compounds in the sample.

In a second series of experiments, sera of diabetic and non-diabetic patients with end stage renal disease (ESRD), known to contain high levels of AGEs, were examined in order to evaluate the non-covalent interaction that characterizes the binding activity of the agents of the present invention. Accordingly, an AGE-binding column was constructed with lysozyme-linked Sepharose beads. The capacity of this lysozyme-matrix was then investigated for specific removal of either *in vitro* generated AGE-Lysine or *in vivo* formed AGEs isolated from sera or peritoneal dialysis fluid of diabetic patients with ESRD (n=10). AGE-lysine was passed over the lysozyme-Sepharose or BSA-Sepharose (control) column and pass-through (unbound) and eluted (bound) fractions were analyzed for protein-crosslinking activity, AGE-immunoreactivity, fluorescence, and brown-colored density. Approximately 60-70% of crosslinking, immunoreactive, and brown-colored species of AGE-lysine were retained by the lysozyme-Sepharose matrix as bound fractions, which could easily be eluted with NaOH (0.1N). In contrast, no fluorescent species of AGE-lysine were associated with this fraction. In addition, no AGE-lysine was retained in the BSA-Sepharose (control) column. Similarly, the lysozyme-Sepharose matrix was found capable of capturing *in vivo* formed crosslinking, AGE-containing species in diabetic sera or dialysis fluid. These, upon elution with NaOH, retained both crosslinking and AGE-activity.

A further experiment was conducted to test the applicability of the invention to remove AGEs from sera of patients with renal failure. Accordingly, chicken lysozyme was linked onto a sepharose matrix (lysozyme-matrix) to enable the capture of AGEs present in serum (sAGE) and dialysis fluid (dfAGE) from diabetic patients with renal failure. Initial studies showed that >80% of ^{125}I-AGE-albumin was retained by the lysozyme-matrix, compared to <10% retained by a control matrix (CL-matrix). More than 60% of desalted AGE-lysine was captured

by lysozyme-matrix and, following elution with 0.1N NaOH, it retained immunoreactivity (by ELISA) and crosslinking activity, but had no intrinsic fluorescence (370/440 nm). Similarly, lysozyme-matrix bound and retained *in vivo* formed sAGE and dfAGE; after passing through the lysozyme-matrix in diabetic sera AGE levels (0.35+0.04 U/mg) were significantly reduced to normal human sera level (0.11+0.02 U/mg; $n=10$, $p<0.0001$), whereas the non-specific protein absorption was <3%. Following elution, lysozyme-bound sAGE- or dfAGE-rich fractions contained high levels of crosslinking AGEs, and promoted large complex formation in a time-dependent manner upon incubation with ^{125}I-BSA, as shown by SDS-PAGE. The formation of this complex was completely prevented by coincubation with aminoguanidine.

Discussion

From the graph depicting the assay results (see Figure 6) of the first series of experiments, the detection of AGE-BSA in an ELISA format based on AGE-binding by lysozyme is clearly demonstrated. The addition of BSA to the sample dilution buffer improved the level of detection of AGE-BSA in the sample, but AGE-modified BSA was detected if NGS was substituted or if no extra protein was included, demonstrating that the assay is capable of such detection. In this method the AGE-binding peptide domain of lysozyme, or an AGE-binding peptide homologous thereto, could be substituted for reduced lysozyme as the capture agent, and such variations are intended to be included within the scope of the invention. Various biological samples contemplated by the present Example, such as, but not limited to, blood, plasma, urine, and various types of tissue fluids or tissue extracts can be readily substituted for the AGE-BSA of the present Example, providing a method to determine the level of AGEs in such samples.

The ability to apply the invention in this manner is illustrated and confirmed in the conclusions that may be drawn from the evaluation of the results of the second series of experiments presented above. Specifically, the data confirm that a matrix such as the lysozyme-Sepharose matrix exemplified above, can capture *in vitro* and

in vivo formed reactive AGEs by non-covalent interactions. This provides a novel approach for the selective depletion of these damaging substances from diabetic uremic serum, and thereby supports the application of the invention to the treatment of uremia and like maladies.

In this connection, the results of the third experiment confirm the therapeutic utility of the lysozyme matrix, as the matrix is demonstrated to be capable of selectively and non-covalently capturing crosslinking AGEs, present in serum or dialysis fluid, and can thus be used to increase AGE removal in patients with renal failure. More importantly, this Example demonstrates that, as a group, the AGE epitopes recognized by the AGE-binding domain of lysozyme are reactive with regard to crosslinking and subject to inhibition by aminoguanidine, immunoreactive with anti-AGE antibodies and non-fluorescent, and thus likely to be relevant to pathogenesis.

This experiment is further confirmatory of the value and operability of the application of the technology to the preparation and use of corresponding devices as set forth above, for a broad range of dialysis procedures. As illustrated, a lysozyme column
is able to reduce elevated serum AGE levels found in association with diabetic renal failure. Thus, the pathogenic *in vivo*-formed AGEs are susceptible to clearance by lysozyme-based absorbents, and lysozyme-derivatized beads as discussed above, can also deplete AGEs from dialysate fluid.

The detection of AGEs in a biological sample by the assay described in this Example is also useful for monitoring the course of anti-AGE therapy and assessing the degree of AGE-modification to proteins for human use or consumption, as well as in other diagnostic applications. Likewise, other known ELISA-like assay formats, where lysozyme, or an AGE-binding peptide domain thereof, substitutes for an AGE-specific antibody, are included within the scope of this Example.

EXAMPLE 4

LOCALIZATION OF AGE-COMPOUNDS TO LYSOZYME-DERIVATIZED SUBSTRATUM AND SPECIFIC ELUTION OF AGE-COMPOUNDS THEREFROM

By immobilizing lysozyme or the AGE-binding peptide portion thereof, i.e. the peptide of the invention, to an affinity chromatographic column (e.g. by derivatizing the beads of the column with lysozyme), it is demonstrated that AGEs can bind to lysozyme, or any molecule with similar AGE binding domain, and be subsequently eluted therefrom with the addition of an appropriate eluant. This method not only provides a useful way to selectively bind AGE-modified molecules, but also provides a means to remove and sequester such AGE-modified molecules from complex mixtures, including biological fluids such as, for example, blood. If desired, the sequestered AGEs can be eluted from the column for use or analysis.

Methods

Cyanogen bromide-activated Sepharose 4B beads were derivatized with lysozyme, according to the manufacturer's instructions, and a 1.5 ml bed volume column was prepared (L-column). Likewise, a control column was established using beads derivatized with BSA (BSA-column). The columns were then loaded with 500 μl of 6 mg/ml AGE-BSA and subsequently washed extensively with PBS. Elution of AGE-BSA from the column was achieved by addition of 0.1 N NaOH and 200 μl fractions were collected. Eluted fractions were neutralized with 1 N HCl.

Results

Figure 7 shows, in U/ml (1 Unit is defined as the competetive activity of a 1:5 dilution of normal human serum against α-AGE antibody binding to an AGE-BSA coated plate), the amounts of AGE-BSA which bound and were eluted from the lysozyme- or BSA-column. AGE-BSA was found to bind to the lysozyme column, which became visibly colored as yellow-brown AGE pigments associated with the lysozyme-derivatized beads, and the AGE pigments and AGE immunoreactivity

eluted as a peak centered at fractions 12-18. It was clear that little or no AGE-BSA bound to the BSA-column (no browned pigments bound to the column to make it visibly colored); there was correspondingly virtually no recovery of AGE immunoreactivity during the elution step.

Discussion

The specificity of AGE binding to lysozyme is evident in the experiments of the present Example. The data demonstrate that AGE-BSA binds to lysozyme which has been chemically attached to chromatography beads. This bound AGE-protein was shown to reversibly dissociate when a suitable eluant was applied. Although NaOH was the eluant used in the present Example any solution capable of causing AGE-modified compounds to be removed from the immobilized lysozyme could be employed, including high tonicity solutions, chaotropic agents, or another AGE preparation. In contrast to data obtained using the lysozyme-column, little or no AGE-BSA was eluted from the BSA-column, further demonstrating that AGE-binding is a specific property of lysozyme and its AGE-binding domain.

The use of such a column as described in this Example provides one skilled in the art with the ability to specifically screen a sample possibly containing AGE-modified compounds by contacting the sample to the column under conditions which can permit binding of AGEs to the column. The applications of such procedure can include, but are certainly not limited to, determination of an amount of AGEs in a sample, partitioning AGEs from a sample as in, for example, hemodialysis, or recovering AGEs from a sample.

Additionally, lysozyme, or a peptide portion thereof capable of binding to AGEs, can be cross-linked to entities other than beads for chromatographic and other uses, for instance, to thereby generate specific targeting agents to localize the conjugate molecule to AGEs. For example, rather than Sepharose beads, a dye or pigment can be attached or conjugated to lysozyme, or the peptide of the invention, and then contacted to AGEs and allowed to bind under appropriate

conditions. The result is the localization of the conjugated molecule to an AGE-modified surface. Any tissue which is manifested with AGEs, such as skin or tooth enamel, can be contacted with such AGE-binding peptide/dye conjugate, for example, to localize the conjugate function to the AGEs. Additionally, a molecule linked to lysozyme or an AGE-binding peptide domain thereof, can be used as a marker for identification of specific tissues containing elevated levels of AGE modifications or AGE-modified compounds.

Colorants that may be useful in the present invention include pigments such as titanium dioxide, as well as other dyes that, for example, may be suitable for food, drug and cosmetic applications, and known as FD&C dyes and the like. Illustrative examples include indigoid dye, known as FD&C Blue No. 2, which is the disodium salt of 5,5'-indigotindisulfonic acid. Similarly, the dye known as FD&C Green No. 1 comprises a triphenylmethane dye and is the monosodium salts of 4-[4-N-ethyl-p-sulfobenzylamino)diphenylmethylene]-[1-(N-ethyl-N-p-sulfoniumbenzyl)-2-5-cyclohexadieneimine]. A full recitation of all FD&C and D&C pigments and dyes and their corresponding chemical structures may be found in the <u>Kirk-Othmer Encyclopedia of Chemical Technology</u>, in Volume 5, pages 857-884, which text is accordingly incorporated herein by reference.

In a further embodiment of the invention, the compounds or constructs described above may be prepared for use in the delivery of active agents or ingredients, such as disinfectants, anti-fungal and anti-microbial agents, and other therapeutics, to the site of an infection, infestation or the like, whether in direct contact with a mammal or not. Accordingly, a compound of this type may comprise the molecule having the hydrophilic loop domain of the invention, together with a particle or bead and the active ingredient of interest. In a specific instance, the compound may be prepared to facilitate the extended or delayed release of the active ingredient, as by the formulation of the bead or the coating thereof with a composition that is limited in solubility or is foraminous, in the latter instance to permit the ratable release of the active as by leaching. Suitable compositions

include pH-sensitive enteric coating materials such as cellulose acetate phthalate, polyvinyl acetate phthalate, hydroxypropylmethylcellulose phthalate, hydroxypropylmethylcellulose acetate succinate, methacrylic acid copolymers, as well as other coating materials such as hydroxyethyl cellulose, hydroxypropyl cellulose, shellac, and mixtures. Naturally, the foregoing list is representative and non-limitative of materials that may be used in the preparation of suitable extended-release formulations.

EXAMPLE 5

OPSONIZATION OF AGE-PROTEINS BY LYSOZYME LEADS TO ENHANCED UPTAKE BY MACROPHAGES

The following illustrates the opsonizing capabilities of the AGE-binding materials and agents of the invention, and specifically provides by way of example a means of removing AGE-compounds from the blood or other tissue of a subject by increasing the uptake of such AGEs by phagocytosis. Thus, by combining AGEs with a suitable opsonin, i.e. the lysozyme molecule of the invention or an AGE-binding peptide domain of or related to the AGE-binding domain of the present invention which is found in lysozyme, it is possible to achieve the opsonization of AGE-modified compounds and thereby enhance the removal of such compounds from a tissue, from the circulation, or from the body. This capability is demonstrated both *in vitro* and *in vivo* below.

Materials and Methods

To determine the rate and extent of uptake of AGE-modified molecules by macrophages *in vitro*, 10^6 mouse macrophage cells (e.g. RAW 264.7 cells) were cultured in a 24-well tissue culture plate containing 1 ml RPMI medium. Two to three μg of ^{125}I labeled lysozyme, -BSA, or -AGE-BSA were next added in conjunction with 50-fold excess of either unlabeled lysozyme, AGE-BSA, or both lysozyme and AGE-BSA. Cells were incubated at 37°C for 2 h and then washed 5 times in RPMI medium. Cells were next removed from the plate by gentle

scraping into microfuge tubes, centrifuged at 400 x g for 5 min. and washed two more times. The washed pellet was examined with a gamma-counter for detection of levels of ^{125}I taken up by the cells. The same protocol was followed with peritoneal macrophages (10^6/well, 2 h, 37°C).

Results

In the presence of lysozyme (12-300 μg/ml) the uptake of AGE-BSA (7.5 μg/ml) was enhanced by 2 to 5-fold while lysozyme had no effect on uptake of unmodified BSA. The enhancement of AGE-BSA uptake was lysozyme dose- and time-dependent and inhibited by excess AGE-BSA. In contrast, lysozyme alone was not significantly internalized under similar conditions. It has also been shown that serum AGE-proteins and AGE-peptides exhibit significant crosslinking activities. Lysozyme abrogated AGE-peptide attachment onto immobilized collagen *in vitro*.

Similarly, as shown in Figure 8, the addition of labeled AGE-BSA to the media allows the AGE-mediated uptake of this substrate by macrophages to be quantified and that AGE-BSA is taken up at an enhanced rate compared to labeled but otherwise unmodified-BSA or lysozyme. Additionally, supplementing either labeled BSA or labeled lysozyme with lysozyme did not result in further uptake of these labeled molecules by macrophage cultures, whereas the addition of lysozyme to solutions of labeled AGE-BSA caused a 2 to 5-fold increase in uptake of AGE-BSA by macrophage cultures. This indicates that lysozyme aids in the uptake of AGE-modified molecules by macrophages and can thereby reduce the levels of the AGE compound in the surrounding media, and thereby further confirms the ability of lysozyme and the other agents of the invention to serve as opsonizing factors to facilitate AGE uptake, and as soluble carriers for the neutralization and removal of circulating reactive AGEs.

As a further test of the effect of lysozyme on macrophage recognition of endogenous serum AGEs, lysozyme was used to construct an AGE-affinity

Sepharose column by which diabetic sera were separated into AGE-rich and AGE-depleted serum fractions. After radiolabeling, aliquots of each fraction were exposed to murine macrophages in the presence or absence of added lysozyme (0.9 mg/ml). The uptake and degradation of the labeled AGE-rich serum proteins by macrophages was significantly enhanced (>3-fold) by lysozyme, compared to control fractions.

To test the effect of lysozyme on the *in vivo* rate of removal of AGEs, AGE-BSA (3mg/day,ip) was injected into healthy rats (n=6) for 7 d, resulting in a 3-fold rise of serum AGEs (from 6±1 to 20±4 U/ml), and was followed by lysozyme (12mg/day, ip) or BSA injection for 1wk. Lysozyme injection resulted in a return of serum AGE levels to normal (8±2, P<0.01) within 3 days, while control BSA injection had no effect.

Discussion

The present example represents an important but previously unanticipated aspect of lysozyme activity which, when applied *in vivo,* can have significant therapeutic value to an individual suffering from deleterious levels of AGEs. The difference between the amount of uptake of labeled AGE-BSA by macrophages when lysozyme is added or omitted from a sample indicates that lysozyme, or a molecule with similar AGE-binding and opsonization activity, can be used to potentiate the phagocytosis of these compounds and thus their removal from blood, tissue, or the body. The net impact would be a decrease in levels of AGE-modified compounds in the tissue or blood, for example, of the individual afflicted with unhealthy amounts of AGEs.

The above experiment provides additional information regarding the opsonizing activity of lysozyme. Specifically, lysozyme participates in the formation of high molecular weight aggregates with AGE-modified proteins, and enhances the uptake of AGE-rich serum fractions by macrophages *in vitro*. Also, lysozyme

administration *in vivo* renormalizes to normal levels circulating AGE levels that were experimentally elevated by prior administration of AGE-BSA.

In summary, the above demonstrates that a hydrophilic cysteine loop-bounded (ABCD motif) in two major naturally existing antimicrobial proteins, lysozyme and lactoferrin, is responsible for AGE-protein binding; binding to AGE blocks lysozyme- and lactoferrin-mediated enzymatic and bactericidal activity. It is postulated that elevated levels of AGEs in diabetic patients may inhibit the bactericidal activity of endogenous antimicrobial proteins, such as lysozyme and lactoferrin. Furthermore, by administering lysozyme, or a peptide with similar AGE-binding capabilities, to individuals suspected of having unhealthy levels of AGEs, it is possible to decrease these harmful levels of AGEs and thereby re-establish the bactericidal activity of the host antimicrobial proteins.

This invention may be embodied in other forms or carried out in other ways without departing from the spirit or essential characteristics thereof. The present disclosure is therefore to be considered as in all respects illustrative and not restrictive, the scope of the invention being indicated by the appended Claims, and all changes which come within the meaning and range of equivalency are intended to be embraced therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LI, YONG MING
VLASSARA, HELEN
CERAMI, ANTHONY

(ii) TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Klauber & Jackson
(B) STREET: 411 Hackensack Avenue
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: NOT YET ASSIGNED
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/418,642
(B) FILING DATE: April 7, 1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 947-1-008 CIP

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201 487-5800
(B) TELEFAX: 201 343-1684
(C) TELEX: 133521

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Cys
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Xaa Cys
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: Internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Xaa Xaa Cys
            20
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: LZ-C1, 62-78

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Cys Asn Asp Gly Arg Ile Pro Gly Ser Arg Asn Leu Cys Asn Ile Pro
1               5                   10                  15

Cys
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: LF-C1, 8-25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly Pro Pro Val
1               5                   10                  15

Ser Cys
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(A) DESCRIPTION: LF-C2, 613-630

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Cys Leu Phe Gln Ser Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr
1               5                   10                  15

Gly Cys
```

WHAT IS CLAIMED IS:

1. A method for treating infection in a subject suspected of having elevated levels of advanced glycosylation endproducts (AGEs) by inhibiting AGE-mediated inactivation of antibacterial proteins, comprising administering a therapeutically effective amount of a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18.

2. The method according to Claim 1, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

3. The method according to Claim 1, wherein n = 15-16.

4. The method according to Claim 1, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

5. The method according to Claim 4, wherein n = 15-16.

6. The method according to Claim 4, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

7. The method according to Claim 1, wherein the antibacterial proteins are selected from the group consisting of lysozyme and lactoferrin.

8. The method according to Claim 1, wherein the molecule is applied topically to a wound, sore, lesion, or ulcer.

9. A pharmaceutical composition for treating infection in a subject suspected of having elevated levels of advanced glycosylation endproducts (AGEs) by inhibiting AGE-mediated inactivation of antibacterial proteins, comprising a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18, in an amount effective to inhibit AGE-mediated inactivation of antibacterial proteins, and a pharmaceutically acceptable carrier.

10. The composition according to Claim 9, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

11. The composition according to Claim 9, wherein n = 15-16.

12. The composition according to Claim 9, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

13. The composition according to Claim 12, wherein n = 15-16.

14. The composition according to Claim 12, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

15. The composition according to Claim 9, wherein the antibacterial proteins are selected from the group consisting of lysozyme and lactoferrin.

16. The composition according to Claim 9, wherein the pharmaceutical carrier is a cream, gel, ointment, or lotion suitable for topical application.

17. A method for partitioning advanced glycosylation endproducts (AGEs) out of a biological sample comprising contacting the biological sample with a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen: Xaa is any L- or D- amino acid; and n = 13-18.

18. The method according to Claim 17, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

19. The method according to Claim 17, wherein n = 15-16.

20. The method according to Claim 17, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid, and n = 13-18.

21. The method according to Claim 20, wherein n = 15-16.

22. The method according to Claim 20, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:3-5 and 7-9.

23. The method according to Claim 17, wherein the molecule is selected from the group consisting of human lysozyme, chicken lysozyme, and lactoferrin.

24. The method according to Claim 17, wherein the biological sample is blood.

25. A composition for partitioning advanced glycosylation endproducts (AGEs) out of a biological sample comprising an amount of a molecule effective to bind AGEs in a biological sample, which molecule has a hydrophilic loop domain having a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1

and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18, and wherein the AGEs can be isolated from the biological sample.

26. The composition according to Claim 25, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

27. The composition according to Claim 25, wherein the molecule is irreversibly associated with a solid phase support.

28. The composition according to Claim 25, wherein the solid phase support is a membrane.

29. The composition according to Claim 28, wherein the membrane is a dialysis membrane.

30. The composition according to Claim 25, wherein n = 15-16.

31. The composition according to Claim 25, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

32. The composition according to Claim 31, wherein n = 15-16.

33. The composition according to Claim 31, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

34. The composition according to Claim 25, wherein the molecule is selected from the group consisting of human lysozyme, chicken lysozyme, and lactoferrin.

35. A device for partitioning advanced glycosylation endproducts (AGEs) out of a biological sample comprising a structure fabricated of an AGE-permeable material, which structure contains particles to which an amount of a molecule effective to bind AGEs in a biological sample is irreversibly associated or immobilized, which molecule has a hydrophilic loop domain having a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18.

36. The device according to Claim 35, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

37. The device according to Claim 35, wherein the AGE-permeable material is polypropylene mesh.

38. The device according to Claim 35, wherein the particles are selected from the group consisting of resin, SEPHAROSE beads, glass beads, plastic beads, and silica gel.

39. A method for treating end-stage renal disease comprising contacting blood from a patient with the composition of Claim 25.

40. A method for treating end-stage renal disease comprising contacting blood from a patient with the composition of Claim 28.

41. A method for detecting the presence of advanced glycosylation endproducts (AGEs) in a sample comprising

a) contacting the sample with a molecule effective to bind AGEs in a biological sample, which molecule has a hydrophilic loop domain having a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1

and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18, under conditions where specific binding of the molecule and AGEs can occur; and

b) detecting binding of the molecule to a component in the sample;

wherein detection of binding of the molecule to a component in the sample is indicative of the presence of AGEs in the sample.

42. The method according to Claim 41, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

43. The method according to Claim 41, wherein the molecule is attached to a solid phase support.

44. The method according to Claim 41, wherein the molecule is labeled.

45. The method according to Claim 41, wherein n = 15-16.

46. The method according to Claim 41, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

47. The method according to Claim 46, wherein n = 15-16.

48. The method according to Claim 47, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:5-9.

49. The method according to Claim 48, wherein the molecule is selected from the group consisting of human lysozyme, chicken lysozyme, and lactoferrin.

50. A method for inhibiting cross-linking of advanced glycosylation endproducts (AGEs) in a subject suspected of having elevated levels of AGEs, comprising administering an amount of a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 residues are capable of forming a bond; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18, effective to bind to AGEs and inhibit crosslinking thereof.

51. The method according to Claim 50, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

52. The method according to Claim 50, wherein n = 15-16.

53. The method according to Claim 50, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

54. The method according to Claim 53, wherein n = 15-16.

55. The method according to Claim 53, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

56. The method according to Claim 50, wherein the antibacterial proteins are selected from the group consisting of lysozyme and lactoferrin.

57. A compound comprising:

a) a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl,

heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18, wherein the molecule is capable of binding to AGEs;

b) conjugated to a marker.

58. The compound according to Claim 57, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

59. The compound according to Claim 57, wherein n = 15-16.

60. The compound according to Claim 57, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

61. The compound according to Claim 60, wherein n = 15-16.

62. The compound according to Claim 60, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

63. The compound according to Claim 57, wherein the marker is selected from the group consisting of radioactive isotopes, enzymes, fluorophores, chemiluminescent agents, paramagnetic molecules, nuclear magnetic resonance shift reagents, colloidal gold, other pigments and dyes, and latex and polystyrene beads.

64. An *in vivo* diagnostic composition comprising the compound according to Claim 57 in a pharmaceutically acceptable carrier.

65. The compound according to Claim 57, wherein said compoud is formulated with a bead or particle, and said compound includes an active ingredient and is adapted for the release of said active ingredient over an extended period of time.

66. An *in vitro* diagnostic composition comprising the compound according to Claim 57 in a carrier suitable for an *in vitro* diagnostic assay.

67. A method for detecting the presence of advanced glycosylation endproducts (AGEs) in a sample comprising

a) contacting the sample with the compound of Claim 57; and

b) detecting binding of the compound to a component in the sample by detecting association of the marker molecule with the component in the sample;

wherein detection of binding of the compound to a component in the sample is indicative of the presence of AGEs in the sample.

68. The compound according to Claim 63, wherein the marker is a white pigment.

69. The compound according to Claim 63, wherein the marker is a pigment or dye selected from the group consisting of indigoid dyes, triphenylmethane dyes, tannin, melanin and mixtures thereof.

70. A cosmetic composition for tooth whitening comprising the compound according to Claim 67 in admixture with a pharmaceutically acceptable carrier selected from gels, pastes, creams, solutions, and dentifrices.

71. A method for whitening teeth comprising applying the composition according to Claim 69 to teeth.

72. A cosmetic composition for creating a tanned appearance comprising the compound according to Claim 68 in an admixture with a pharmaceutically acceptable film-forming topical carrier.

73. A method for creating a tanned appearance comprising applying a composition according to Claim 71 to skin.

74. A method for removing a marker molecule conjugate from a surface that has been coated with a composition containing the marker molecule conjugate of Claim 57, comprising applying to said surface a cleaning composition containing an AGE, whereby the AGE in said composition is capable of competitively binding with said marker molecule conjugate and thereby enabling said marker molecule conjugate to be removed from said surface.

75. The method according to Claim 73, wherein said cleaning composition is a liquid.

76. The method according to Claim 73, wherein said cleaning composition is selected from a granular solid, a gel, a paste, a solution and a suspension.

77. A method for assessing the likelihood and severity of the onset and development of a disease, disorder or dysfunction in a host, in which the presence and level of AGEs is associated, comprising measuring the presence and activity in a biological sample taken from said host of a molecule having an hydrophilic loop domain, which hydrophilic loop domain has a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18.

78. The method according to Claim 76, wherein said Z_1 and Z_2 residues are bonded to form a cross-link.

79. The method according to Claim 76, wherein n = 15-16.

80. The method according to Claim 76, wherein the hydrophilic loop domain is $R_1CysXaa_nCysR_2$ (SEQ ID NOS:1-6), Xaa is any L-amino acid and n = 13-18.

81. The method according to Claim 79, wherein n = 15-16.

82. The method according to Claim 76, wherein the hydrophilic loop domain is selected from the group consisting of SEQ ID NOS:7-9.

83. A conmposition for the delivery of an active agent comprising a structure fabricated of an AGE-permeable material, which structure contains particles to which an amount of a molecule effective to bind AGEs in a biological sample is irreversibly associated or immobilized, which molecule has a hydrophilic loop domain having a structure corresponding to $R_1Z_1Xaa_nZ_2R_2$ (SEQ ID NOS:1-6), wherein Z_1 and Z_2 are residues capable of forming a cross-link; R_1 and R_2 are independently a polypeptide, a C_1 to C_{12} alkyl, aryl, heteroalkyl, or heteroaryl group, or hydrogen; Xaa is any L- or D- amino acid; and n = 13-18.

FIGURE 1

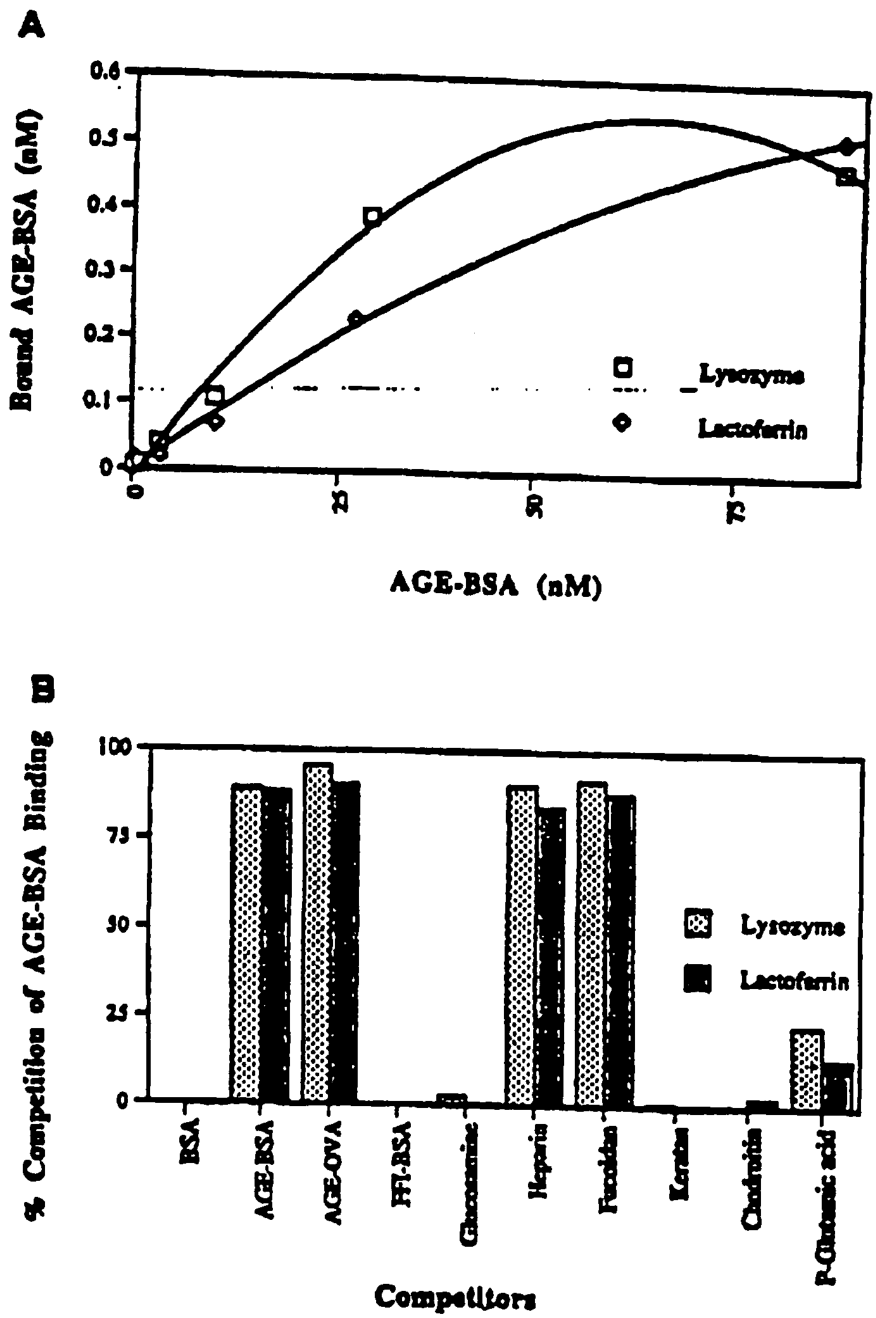

A
0.6
0.5
0.4
0.3
0.2
0.1
0
Bound AGE-BSA (nM)
0
25
50
75
AGE-BSA (nM)
Lysozyme
Lactoferrin
B
% Competition of AGE-BSA Binding
100
75
50
25
0
Lysozyme
Lactoferrin
BSA
AGE-BSA
AGE-OVA
FFI-BSA
Glucosamine
Heparin
Fucoidan
Keratan
Chondroitin
P-Glutamic acid
Competitors

FIGURE 2

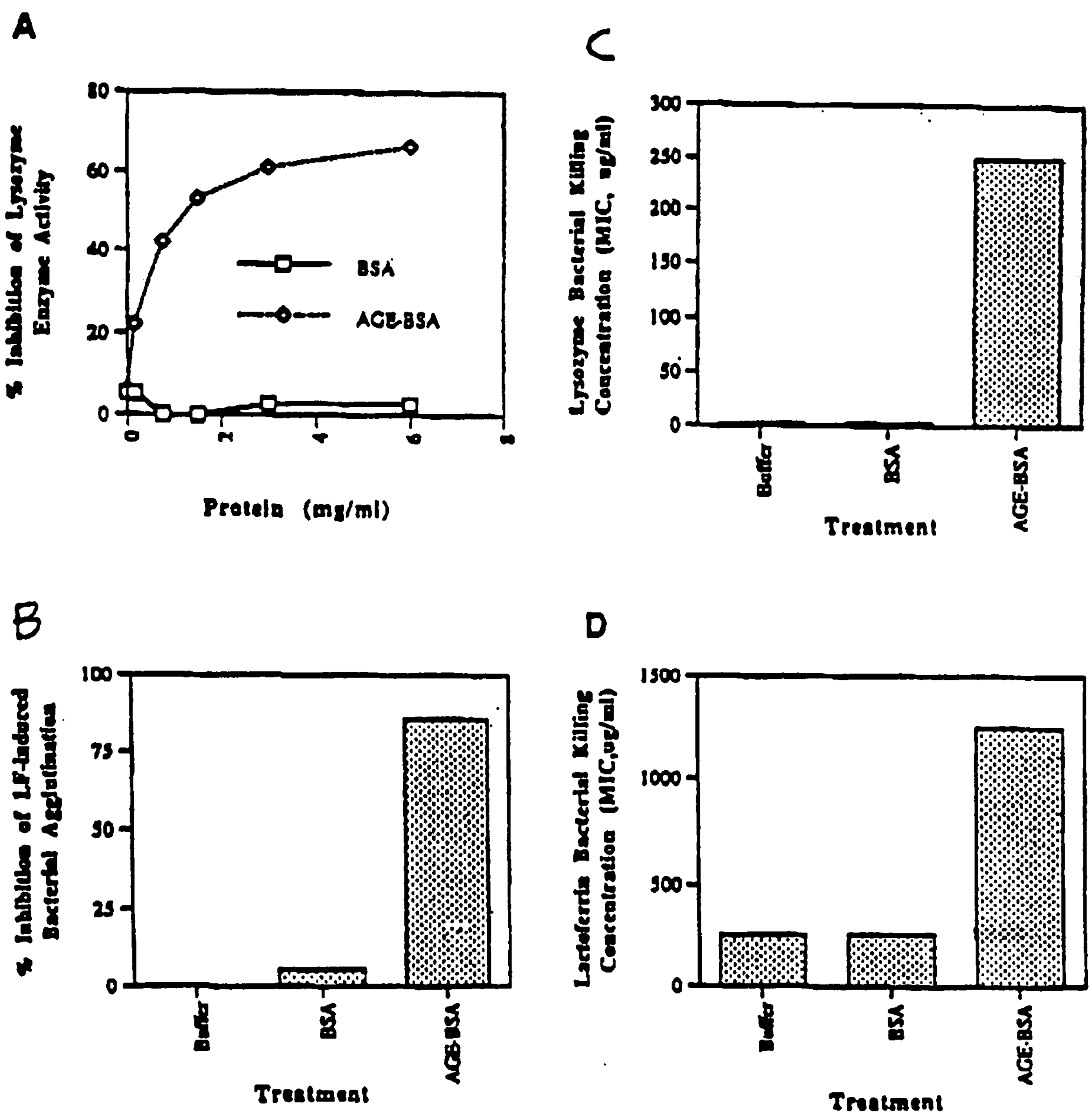

A
% Inhibition of Lysozyme Enzyme Activity
80
60
40
20
0
0
2
4
6
8
BSA
AGE-BSA
Protein (mg/ml)
C
Lysozyme Bacterial Killing Concentration (MIC, ug/ml)
300
250
200
150
100
50
0
Buffer
BSA
AGE-BSA
Treatment
B
% Inhibition of LF-induced Bacterial Agglutination
100
75
50
25
0
Buffer
BSA
AGE-BSA
Treatment
D
Lactoferrin Bacterial Killing Concentration (MIC,ug/ml)
1500
1000
500
0
Buffer
BSA
AGE-BSA
Treatment

FIGURE 3

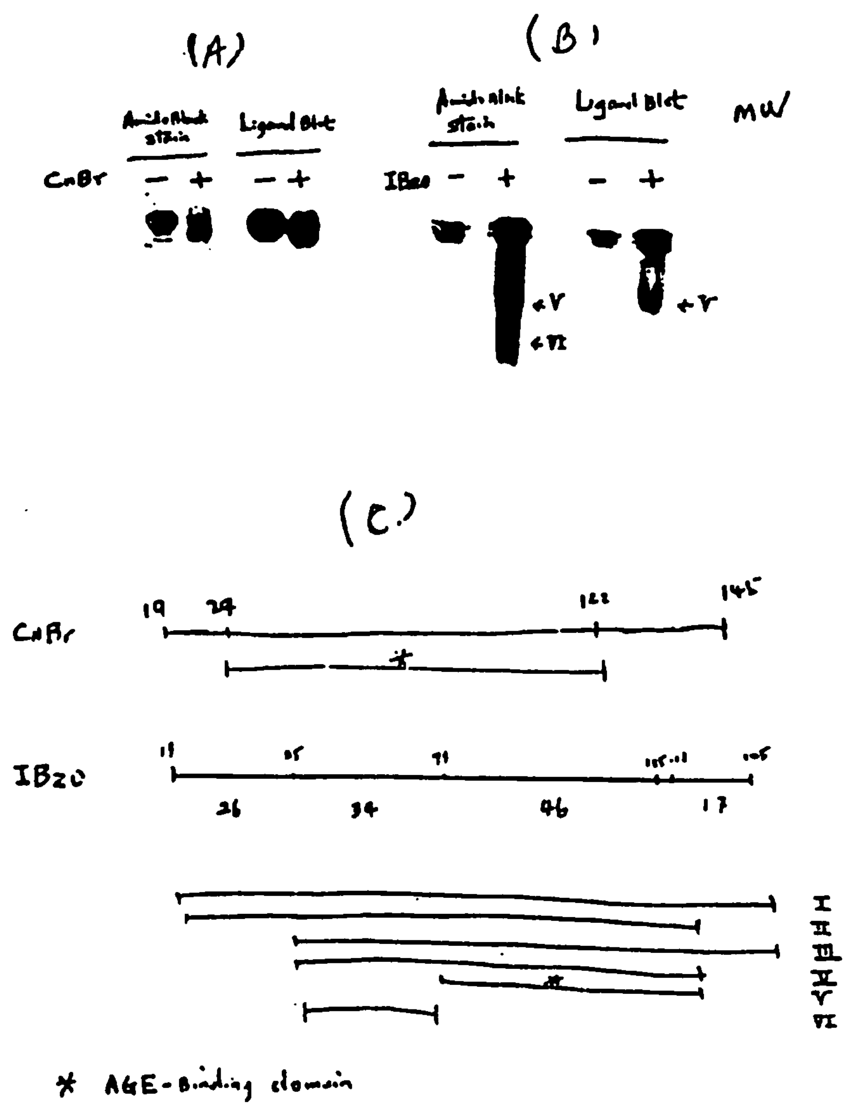

(A)
(B)
Ligand Blot
Ligand Blot
MW
CnBr
– +
– +
– +
– +
← V
← VI
← V
(C)
CnBr
19
24
122
145
*
IBzo
26
34
46
17
I
II
III
IV
V
VI
* AGE-binding domain

FIGURE 4

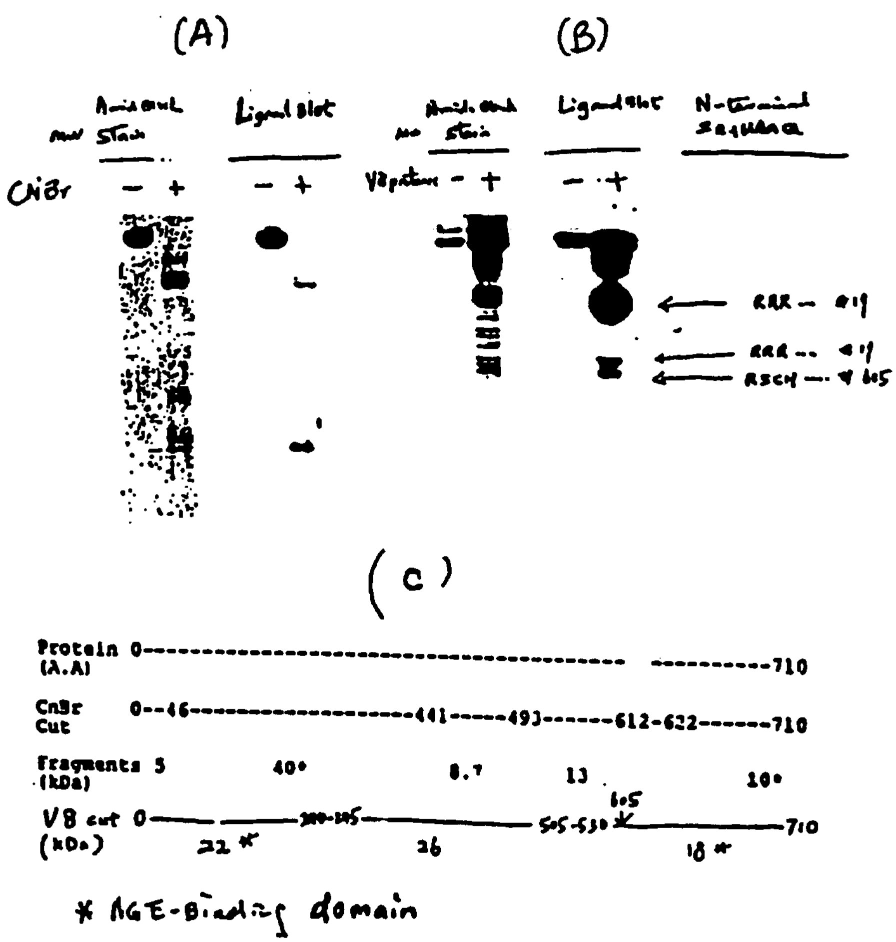

(A)
(B)
Ligand blot
CNBr - +
- +
- +
- +
(C)
Protein 0--710
(A.A)
CnBr 0--46--------------------441------493-------612-622-------710
Cut
Fragments 5 40* 8.7 13 10*
(kDa)
V8 cut 0 505-530 605 710
(kDa) 22* 26 18*
* AGE-Binding domain

FIGURE 5A

LZ-C1 62 CNDGRIPGSRNLCNIPC 78

LF-C1 27 CFQWQRNMRKVRGPPVSC 46

LF-C2 632 CLFQSETKNLLFNDNTEC 649

FIGURE 5B

FIGURE 5C

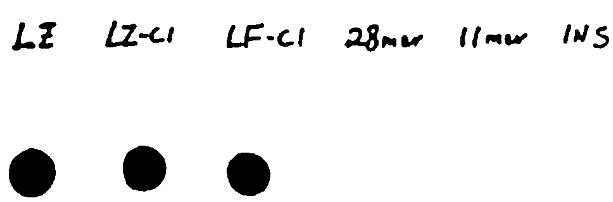


Figure 6

AGE-BSA binding assay to c-LZ(reduced) on plate
using a-AGE monoclonal ab 2/27/95

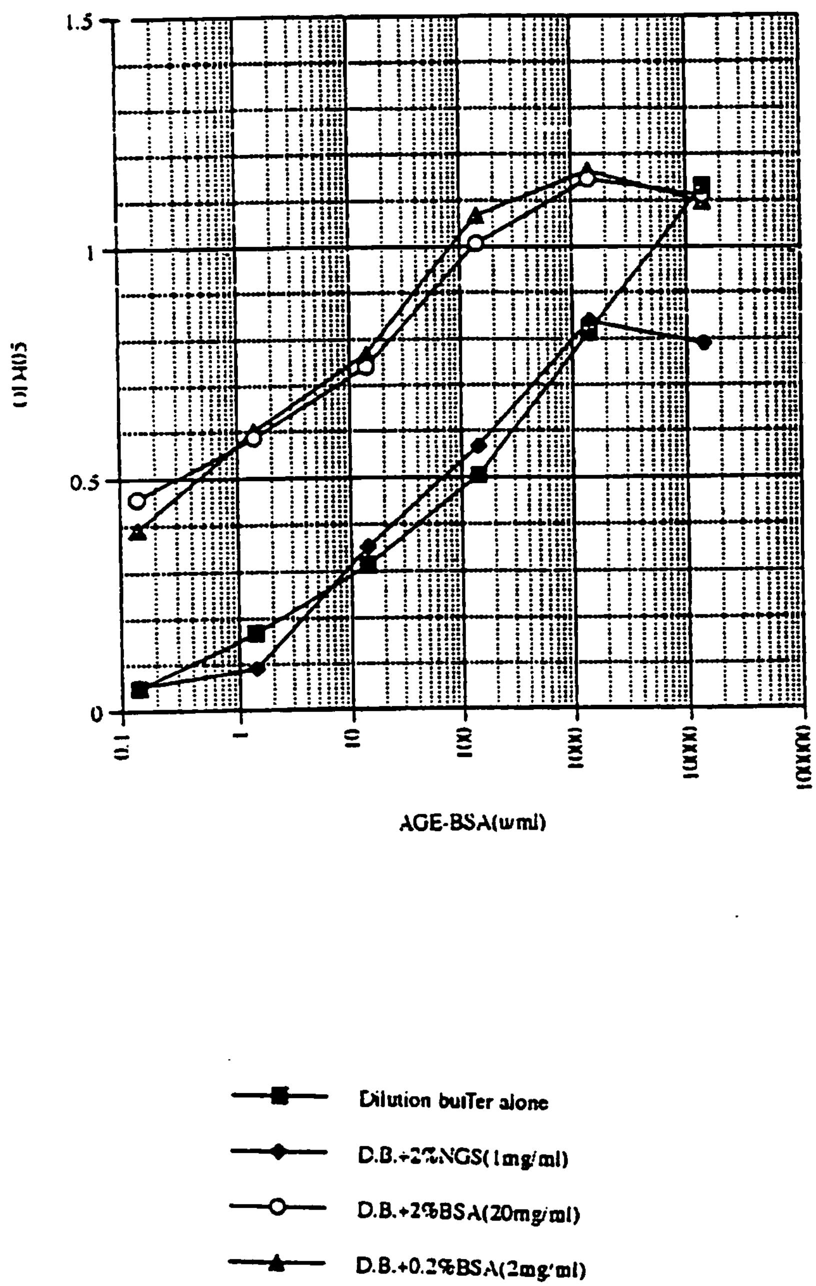


Figure 7

AGE(u/ml) in fractions of AGE-BSA eluted with 0.1N NaOH from BSA and LZ column (by a-AGE-RNase) 1/10/95

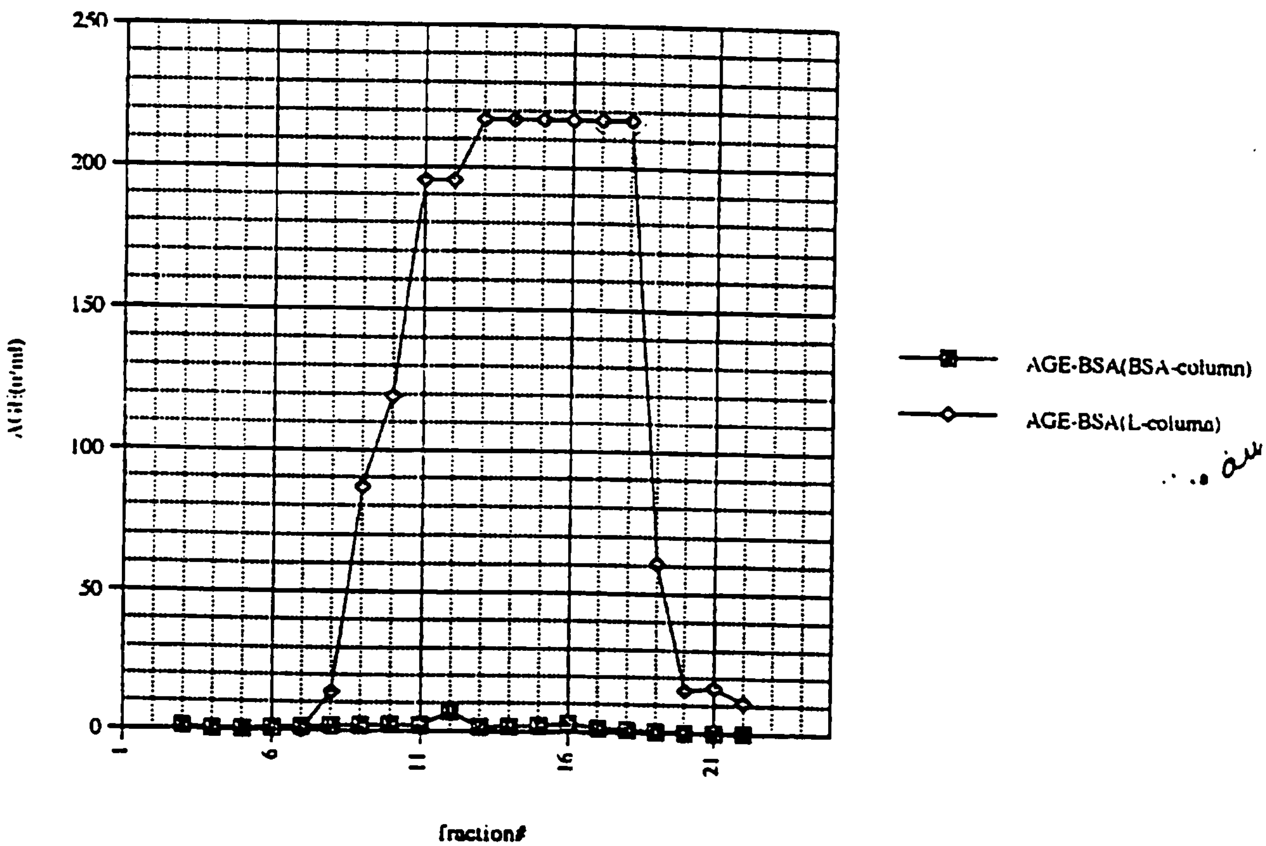
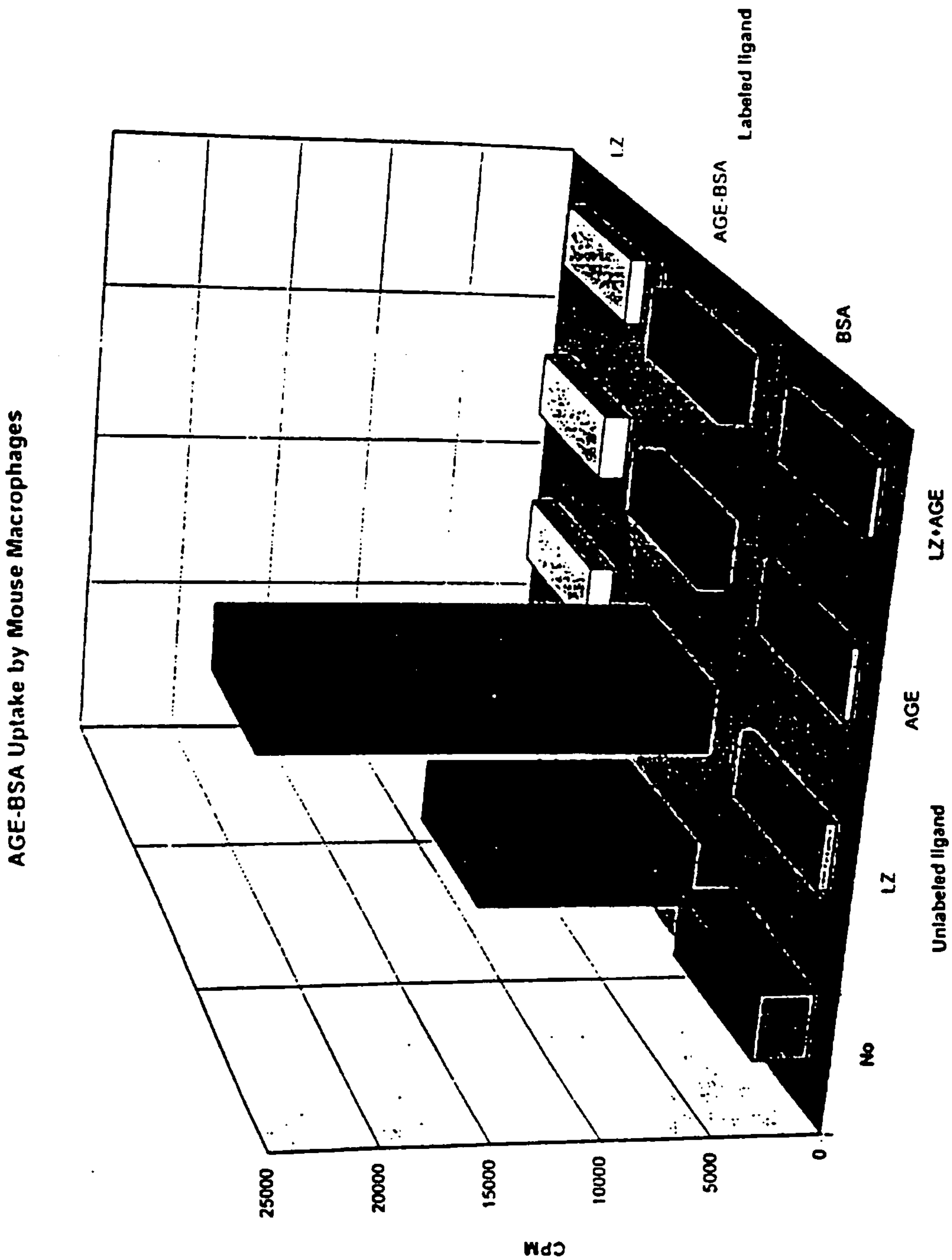


Figure 8


AGE-BSA Uptake by Mouse Macrophages
CPM
25000
20000
15000
10000
5000
0
No
LZ
AGE
LZ•AGE
BSA
Unlabeled ligand
AGE-BSA
LZ
Labeled ligand

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/04755

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C07K14/79 A61K38/40 G01N33/68 A61K7/16 A61K7/42

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP,A,0 629 347 (MORINAGA MILK INDUSTRY CO LTD) 21 December 1994 Seq.ID's 22-30 see claims; examples ---	1-5, 7-13,15, 16
X	EP,A,0 474 506 (MORINAGA MILK INDUSTRY CO LTD) 11 March 1992 see page 6, line 45 - page 7, line 12; examples ---	1-5, 7-13,15, 16
A	WO,A,93 04086 (UNIV ROCKEFELLER) 4 March 1993 see claims; examples --- -/--	17-67

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

2

Date of the actual completion of the international search	Date of mailing of the international search report
2 September 1996	06.09.96

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	Fuhr, C

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/04755

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	WO,A,95 20979 (PICOWER INST MED RES ;VITEK MICHAEL P (US); CERAMI ANTHONY (US); B) 10 August 1995 see page 11, line 29 - page 12, line 31; claims; examples ---	1,9,41, 50
A	JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 268, no. 20, 15 July 1993, BALTIMORE, MD US, pages 14940-14947, XP002012251 R.N. KNIBBS ET AL.: "Carbohydrate-binding Protein 35" see page 14941, left-hand column, paragraph 7 - right-hand column, paragraph 1 see page 14942, right-hand column, paragraph 4 - right-hand column, last paragraph see page 14945, left-hand column, paragraph 2 - page 14947, left-hand column, paragraph 2 -----	1,25

2

INTERNATIONAL SEARCH REPORT	mational application No. PCT/US 96/04755

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Please see Further Information sheet enclosed.

2. [ ] Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. [ ] As all searchable claims could be searches without effort jusufying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

International Application No. PCT/US96/04755

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

Remark : As far as claims 1-8, 39-40, 50-56, are directed to a method of treatment of (diagnostic method practised on) the human/animal body the search has been carried out and based on the alleged effects of the compound/composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Inter   nal Application No
PCT/US 96/04755

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
EP-A-0629347	21-12-94	JP-A-	5320067	03-12-93
		AU-B-	665381	04-01-96
		AU-B-	2956492	01-09-93
		CA-A-	2128612	05-08-93
		WO-A-	9314640	05-08-93
		JP-A-	5310594	22-11-93
EP-A-0474506	11-03-92	JP-A-	5092994	16-04-93
		AU-B-	645342	13-01-94
		AU-B-	8370491	12-03-92
		US-A-	5304633	19-04-94
WO-A-9304086	04-03-93	US-A-	5202424	13-04-93
		AU-B-	2506792	16-03-93
		US-A-	5316754	31-05-94
WO-A-9520979	10-08-95	AU-B-	1870195	21-08-95